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(54) **GENE SIGNATURE.**

(57) A 3'-directed cDNA library which accurately reflects the abundance ration of mRNA in a cell has been prepared from various human tissues, and sequencing of the cDNAs contained in the library has be conducted to examine the incidence of each cDNA in each tissue. As each cDNA has expression information with each tissue corresponding to the mRNA concentration, these cDNAs are usable as a probe or primer for detecting cell anomaly or discriminating cells. The cloned gene can produce porteins utilizable as a medicine or the like.

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## Fields of the Invention

The present invention relates to purified single-stranded DNA molecules, purified single-stranded DNA molecules complementary thereto or purified double-stranded DNA molecules consisting of said single-stranded DNA molecules, which can specifically hybridize to human genomic DNA, human cDNA or human mRNA at particular sites. The DNA molecules of the present invention can be used for detecting the overall or individual expression status of mRNAs coding for the corresponding cellular proteins, detecting and diagnosing cellular abnormalities due to disease and viral infection, or distinguishing and identifying the cell type, and efficiently cloning genes expressed in a tissue-specific manner. The present invention further includes cloned DNA molecules which can be used to produce proteins useful as pharmaceutical products or the like.

## Related Arts

Recognizing the importance of the most fundamental attribute of mRNA, that is, "the nature of the cell is determined by the expression pattern of genes as reflected in the population of mRNA", the inventors of the present invention have proposed "body mapping" as a unique approach to their objective. This is an entirely novel attempt to prepare "the information on gene expression" for presumably about 200 different kinds of cells and tissues present in the human body and elucidate when, where and to what extent a certain gene is expressed, and map genes to the respective organ or cell type in which they are expressed.

While a variety of cells in the living body express various proteins depending on their respective biological functions, the intracellular concentrations of these proteins vary according to the cell type, stage of development and differentiation, environment, etc.

In general, genes are classified into "genes encoding proteins essential for the life of the cell" and "genes encoding proteins responsible for functions specific to the cell". Of these two, "genes encoding proteins essential for the life of the cell" are expressed constantly in all types of cells and also called "housekeeping genes", while "genes encoding proteins responsible for functions specific to the cell" are often expressed specifically in a particular type of cells or a particular group of cells, and also may be specifically expressed at a particular stage of cellular development and differentiation. Furthermore, they are often "inducible genes" and the amount of their expression varies depending upon the environment to which cells are exposed. In other words, cells may grow as a result of the expression of "genes encoding proteins essential for the life of the cell" and display their specific functions as a result of the expression of "genes encoding proteins responsible for functions specific to the cell".

However, under abnormal cellular conditions due to disease or infection, the expression of genes within individual cells is altered as compared with that under the normal conditions. Especially, during viral infection, RNAs encoding virus-specific proteins are synthesized in large amounts within the cell, leading to the production of said protein in large amounts. In other words, the alteration in the expression level of genes within the cell, especially as reflected in the concentration of intracellular mRNA, can lead to such abnormal cellular conditions as seen in diseases.

Thus, the function of each cell in the living body is closely related to the expression status of genes within the cell. Accordingly, in order to elucidate the function of each cell at molecular level or to investigate the pathogenesis of a disease at molecular level, it becomes necessary to comprehend the expression status of cellular genes, especially the intracellular concentration of each mRNA.

A theoretically possible approach to this objective is the extraction and analysis of all cellular proteins for determination of expression status. However, although it may be possible to isolate a specific protein, in most cases it is almost impossible to completely isolate all of these proteins, because a great variety of proteins are expressed within the cell.

Another approach is to directly estimate the concentrations of cellular mRNAs corresponding to all intracellular proteins. However, although it may be possible to isolate a specific mRNA, it is practically impossible to completely isolate all of these mRNAs and directly estimate their amounts, because a great variety of mRNAs are synthesized simultaneously within the cell and furthermore they may be unstable and susceptible to enzymatic degradation during their extraction.

This invention aims to provide DNA molecules which can be used as probes or primers required for detecting the overall or individual expression status of mRNAs coding for the corresponding cellular proteins, detecting or diagnosing cellular abnormalities due to disease or virus infection, recognizing and identifying various cell types, and efficiently cloning genes expressed in a tissue-specific manner. Moreover, the present invention aims to provide cloned DNA molecules which can be used to produce proteins useful as pharmaceutical products.

## Summary of the invention

In general, the genetic information flows in order from DNA to mRNA and to protein (F. H. C. Crick, 1958). That is, "the information for the amino acid sequence of a protein" is first transcribed into mRNA and then translated into protein.

To explain this in further detail mammalian genes commonly comprise a region encoding a protein and a region regulating the expression of said gene. The regions of a gene encoding protein (called "exons") are often separated by intervening sequences (called "introns"). When a gene is transcribed into RNA, the introns of the precursor RNA (pre-mRNA) are excised and exons are connected in tandem to form a contiguous structure coding for a particular protein (this process is called "splicing"). On the other hand, the region regulating the expression of gene comprises, in addition to the regions directly regulating transcription such as a promoter and operator which are present upstream of the transcription region, untranslated regions are located both upstream (5') and downstream (3') of the coding region. In particular, 3' untranslated region (3' UTR) is important for regulating expression, since it contributes to the transport and stability of mRNA. During the processing of pre-mRNA, a methylated cap is added at its 5' end, the 3' untranslated region is cleaved at a specific site, a poly(A) tail is attached by adding 100 - 200 adenylate residues to the cleaved end, and the coding regions are spliced together to form mRNA. The protein is then synthesized after attachment of ribosomes to the mRNA.

The inventors of the present invention have elucidated that, in general, when the intracellular level of a particular mRNA is high, the expressed amount of the corresponding protein is also elevated, and also that it is possible to estimate the relative concentration of each intracellular protein by estimating relative intracellular concentration of the corresponding mRNA [DNA sequence 2, 137-144 (1991); Nature genetics, 2, 173-179 (1992)].

Basically in the present invention, mRNA is extracted from a particular cell and cDNA is synthesized by conventional methods using reverse transcriptase. However, in the present invention, cDNA is synthesized using a method developed by the inventors of the present invention so as to reflect the relative intracellular concentration of mRNA. A cDNA library is constructed and a group of cDNAs representing the population of total mRNA are cloned and sequenced.

An approach which appears to be similar to the one used by the inventors of the present invention but is entirely different, is the method of cloning of a cDNA library constructed by the random priming by Venter et al.

Venter's group randomly cloned cDNAs from commercially available cDNA libraries derived from brain cells (catalog No. 936206, 936205 or 935, Stratagene, California) and determined their base sequences [Science 252, 1651-1656 (1991); Nature 355, 632-634 (1992)].

While the method used by Venter et al. involves sequencing of cDNAs obtained by random priming, this method has the following drawbacks:

- 1) Since random cloning of various regions of a single-stranded mRNA may often lead to the formation of many cDNA fragments without any mutual overlapping portions, it is difficult to determine whether these cDNA fragments are derived from the same mRNA or a different one,
- 2) The longer a mRNA strand, the higher the chance for said mRNA to be reverse-transcribed into cDNA, and
- 3) Since the availability of each primer to be used among random primers differs depending on their base sequences, the relative frequency of cDNA synthesis is variable.

From aforementioned reasons, the relative frequency of appearance of cDNA does not reflect the relative concentration of cellular mRNA. Consequently, it is impossible to determine the relative concentration of each mRNA and the actual population of intracellular proteins by using the method of Venter et al.

However, with the method developed by the inventor of the present invention, it is possible to construct a cDNA library which precisely reflects the relative concentration of mRNA without any of the aforementioned complications. Since, in the present invention, cDNA is synthesized using only "poly-T" as the primer, the 3' ends of the cDNA have "a poly A tail". Therefore, the synthesis of cDNA with "poly-T" as the sole primer is initiated from the 3' end resulting in the formation of 3'-oriented cDNA. Since the 3' untranslated sequence is unique to a particular mRNA species and not present in other mRNA species [Birnstiel, M. L., et al., Cell 41, 349-359 (1985)], almost all the 3' end-oriented cDNAs hybridize with specific mRNAs. Digestion of the resulting cDNA with a restriction enzyme MboI which recognizes the specific four-base sequence GATC results in the formation of cDNA extending from the 3'-terminus to the first MboI restriction site. In the present invention, each cDNA thus cloned and included in "a cDNA library faithfully reflecting the relative intracellular concentration of mRNA" is called a "gene signature" (abbreviated as GS hereinafter). A GS includes not only the double-stranded DNA but also each single-stranded DNA thereof.

The present invention relates to a purified single-stranded DNA, purified single-stranded DNA complementary thereto, or a purified double-stranded DNA consisting of said single strands, containing all or a portion of a single-stranded DNA (or a single-stranded DNA complementary thereto) comprising any of the base sequences listed under the sequence identification number (SEQ ID NO) 1 - 7837 and hybridizing specifically to a particular site of human genomic DNA, human cDNA or human mRNA. The present invention also relates to probes and primers consisting of said single-stranded DNA. The present invention also relates to a purified single-stranded DNA, a purified single-stranded DNA complementary thereto, or a purified double-stranded DNA consisting of said single strands, containing all or a portion of a single-stranded DNA (or a single-stranded DNA complementary thereto) which is complementary to a human mRNA containing any of the base sequences listed under SEQ ID NO 1 - 7837 ( wherein T is read as U ) or any portion thereof at its 3' region and hybridizing specifically to a particular site of human genomic DNA, human cDNA or human mRNA. The present invention also relates to probes and primers consisting of said single-stranded DNA.

The present invention is explained further in detail as follows.

The DNA of the present invention not only includes a single-stranded DNA (or a single-stranded DNA complementary thereto) comprising any of the base sequences listed under SEQ ID NO 1 - 7837 but also includes a single-stranded DNA containing a portion of said single-stranded DNA (or said single-stranded DNA complementary thereto) if it hybridizes to human genomic DNA, human cDNA or human mRNA.

Furthermore, the DNA of the present invention not only includes a single-stranded DNA (or a single-stranded DNA complementary thereto) which is complementary to a mRNA containing any of the base sequences listed under SEQ ID NO 1- 7837 (wherein T is read as U) or any portion thereof at its 3' region but also includes a single-stranded DNA (or a single-stranded DNA complementary thereto) containing a portion of said single-stranded DNA (or said single-stranded DNA complementary thereto) if it hybridizes to human genomic DNA, human cDNA or human mRNA.

In addition, the DNA of the present invention not only includes a single-stranded DNA or a single-stranded DNA complementary thereto but also includes a double-stranded DNA consisting of said single strands.

Obviously, the term "contain" as used herein does not necessarily mean that the DNA of the present invention contains at a single site without interruption (1) "a single-stranded DNA (or a single-stranded DNA complementary thereto) comprising any of the base sequences listed under SEQ ID NO 1-7837 or a portion thereof" or (2) "a single-stranded DNA (or a single-stranded DNA complementary thereto) which is complementary to a mRNA containing any or any portion of the base sequences listed under SEQ ID NO 1 - 7837 (wherein T is read as U) at its 3' region or a portion of said single-stranded DNA." In other words, the term "contain" is applicable also to the case where one or more exogenous bases are inserted in the base sequence of the DNA (1) or (2).

The hybridization to a particular site of human genomic DNA, human cDNA or human mRNA can be achieved under standard conditions (see e.g., *Molecular Cloning: A Laboratory Manual*, Sambrook, J., et al., Cold Spring Harbor Laboratory Press, 1989). In the following preferred embodiment, there will be described methods for constructing a cDNA library which reflects precisely the relative intracellular concentration of mRNA, cloning cDNA groups which correspond to total mRNA, and determining the base sequence of each cDNA.

First, cells from specific tissues, for example, cells from organs, for example, cells derived from human liver (HepG2) are grown, and the total mRNA is extracted by standard procedures. mRNA thus obtained is attached to a vector to construct a cDNA library.

For example, mRNA is attached to the vector plasmid pUC19, which has the M13 sequences flanking the cloning site, as follows.

pUC19 is cleaved by HincII and PstI and poly-T of 20 bp - 30 bp is added to the PstI-digested end to which the 3'-end poly-A tail of the mRNA is hybridized (Fig. 1a). After the DNA strand is extended with conventional methods using reverse transcriptase, a double stranded DNA is formed with DNA polymerase (Fig. 1b). The double stranded DNA thus obtained is cleaved with the restriction enzyme MboI which recognizes a specific four base sequence (Fig. 1c).

MboI, which recognizes a four base sequence (GATC), cleaves the DNA within a few hundred bases from the poly-A tail. Since MboI is found to digest, without exception, about 300 human cDNAs which were randomly selected from the GenBank data base by the inventor of the present invention, this enzyme cleaves the cDNA to be cloned at a specific site. In addition, as pUC19 is prepared in *dam*<sup>+</sup> *E. coli*, e.g., *E. coli* JM109 and since its adenine at the MboI recognition site is methylated (G<sup>m</sup>ATC), it is not cleaved by MboI.



Subsequently, in order to prepare a vector containing the double-stranded DNA which has previously been attached to pUC19 and has the MboI-cleaved end, the pUC19 DNA is digested with BamHI to make termini cohesive with the MboI-cleaved end. Since the recognition sequence of BamHI (GGATCC) contains that of MboI (GATC), the extended portion of the double-stranded DNA is not cleaved with BamHI.

5 The resulting double-stranded DNA is then circularized by standard ligation methods, and the recombinant vector plasmid thus prepared is introduced into *E. coli*, e.g., *E. coli* DH5 in order to make a cDNA library.

With this method, only a clone containing the base sequence upstream of the poly-A tail of the mRNA is obtained.

10 Since the average size of the inserted cDNA fragment is relatively small, 270 bp, it is free from biased cloning resulting from variations in the efficiency of cDNA synthesis and transformation that occur in the case of larger sized DNAs. Furthermore, because instability due to repeated base sequences and the like is eliminated, the cDNA library of the present invention faithfully represents the relative concentration of mRNA in the cell.

15 Furthermore, when the cDNA inserted into the vector is relatively short, it is possible to accurately amplify the cDNA fragment using the sequence of the vector flanking it as a primer. It is also possible to determine the base sequence from the 5' end directly by the PCR without interference from the 3' poly-A tail which will reduce the accuracy of sequence determination.

Amplification of the GS, i.e., the cDNA fragment inserted into the vector, is performed as follows.

20 The *E. coli* cells in which the cDNA library is introduced are grown using standard methods and lysed. Debris contained in the bacterial lysate are removed by centrifugation and the supernatant containing the vector DNA is recovered. The vector DNA thus obtained is used as the DNA template for amplification by the PCR (Fig. 1d, amplification with PCR primers 1 and 2).

Base sequences flanking both ends of the GS is properly selected for use as primers and the PCR is performed under standard conditions. PCR products thus obtained are subjected to the elongation reaction using fluorescence primers complementary to the vector sequence flanking the 5' end of the GS, and the sequence is determined with an autosequencer (Fig. 1d, sequence determination with dye primer).

Based on the results of the sequence determination of each GS, the species and the frequency of appearance of the GS in each tissue or cell type are analyzed.

30 As to each cell type not only normal cells but also cells under pathogenic conditions (such as tumor cells, virus infected cells, etc.) can be used without any restriction. For example, liver cells (from fetus, neonate or adult), various hematopoietic cells (granulocytic, monocytic, etc.), lung cells, adipocytes, endothelial cells, osteoblasts, colon mucosa cells, retinal cells and hepatoma cells (HepG2, etc.), and promyelocytic leukemia cells (HL60, etc.) will be used. The appearance frequency for each GS is described for each cell type in Tables 1 through 219. There, patent number represents "SEQ ID NO for each GS", size represents the "length of each GS", and F represents the "sum of appearance frequencies in the cells studied". In addition, hepG2 stands for "hepG2 (a liver cancer cell line)", HL60 stands for "HL60 promyelocytic leukemia cell line", granulo stands for "granulocytoid, HL60 stimulated by DMSO", mono stands for "monocytoids, HL60 stimulated by TPA", 40 w liver stands for "40 w neonatal liver", 19 w liver stands for "liver of a 19 weeks old fetus, adult liver is "adult liver", lung stands for "adult lung", adipose stands for "subcutaneous adipose tissue", endothel stands for "primary cultured aortic endothelium", osteoblast stands for "primary cultured osteoblast", colon mucosa is "colon mucosa", small cell carci stands for "small cell carcinoma of lung", retina is "retina", cerebral cortex is "cerebral cortex", adenocarci (lung) stands for "adenocarcinoma of lung", squamous cell ca (lung) stands for "squamous cell carcinoma of lung", keratinocyte stands for "primary cultured keratinocyte", fibroblast stands for "primary cultured fibroblast", Alzheimer stands for "Alzheimer temporal lobe", cerebellum stands for "cerebellum", visceral fat is "visceral fat", corneal epithelium is "corneal epithelium", peripheral granulocyte is "peripheral granulocyte", neuroblastoma is "neuroblastoma" and taste bud of tongue is "taste bud of tongue".

"Accession number of target mRNA" represents the accession number of the entry in GenBank 50 Release 79 whose base sequence has homology with that of each GS, "match %" represents the percent homology of the GS sequence relative to that of said homologous sequence, "match starts at (GS)" represents the base position counted from the 5'-end of the GS at which the region for homology calculation starts, "match starts at (GenBank)" represents the base position counted from the 5'-end of the GenBank sequence at which the region for homology calculation starts, and "GenBank target size" 55 represents the whole length of the GenBank sequence corresponding to the GS. The columns in Tables 1 - 219 represent the same items as in Table 1.

Based on the data in Tables 1 - 219, each GS can be classified into several groups. A GS, which is expressed at high frequency in a specific cell or groups of cells with similar property, for example,

promyelocytic leukemia cell, granulocyte and monocyte and not expressed entirely or expressed very little in other cells (groups), is a likely GS corresponding to the gene encoding "the protein responsible for functions specific to the cell" (e.g., GS0001553, GS0002047, GS004895, etc.). On the other hand, a GS, which is expressed commonly in every kind of cell, most likely corresponds to the gene encoding "the protein essential for the life of the cell" (e.g., GS0000019, GS0000155, GS0000861, etc.). In addition, some GSs are expressed at low frequency (e.g., GS0000013, GS0002399, GS0003155, etc.).

Since the GS with the sequence determined as described above will reflect the population of mRNA expressed in a particular cell, it must be possible to find the relative concentration of mRNA in each cell by determining the appearance frequency for each GS in a cDNA library derived from that cell. Therefore, to confirm the correlation between the appearance frequency for each GS in a cDNA library and the relative concentration of cellular mRNA, the GS thus obtained was labeled with  $^{32}\text{P}$  by standard methods and used as the probe in the following hybridization test. mRNA isolated from a specific cell is hybridized to said  $^{32}\text{P}$ -labeled probe under standard conditions. The results of this Northern hybridization test were such that, when a GS found with high appearance frequency in a cDNA library was used as a probe, a dense band was formed, confirming the correlation of the frequency of appearance of the GS with the relative concentration of mRNA in the cell (see Example 5).

Similarly, the colony hybridization test of the cDNA library constructed as described above with a  $^{32}\text{P}$ -labeled probe prepared as described above showed a close correlation between the frequency of appearance of the GS and the number of colonies hybridized with said GS (see Example 6), confirming the correspondence of the frequency of appearance of the GS and relative concentration of the GS in a cDNA library.

From the above results, by determining the appearance frequency of each GS in a cDNA library derived from a variety of cells, it has become possible to determine the expression status of the gene (or mRNA) corresponding to each GS. This fact implies conversely that each GS may be useful for industrial purposes as a specific probe or primer encoding information about the expression status of its corresponding gene (or mRNA) for each cell. For example, when it is proven that "a certain GS appears at high frequency only in a cDNA library derived from tissue A, that is, the gene corresponding to said GS is specifically expressed only in tissue A", by conventional cloning of the corresponding full-length cDNA using said GS as a probe or primer, it is possible to clone a full-length gene which is expressed in a tissue-specific manner.

Furthermore, for example, when it is proven that "the frequency of appearance of a certain GS is low in a cDNA library derived from tissue B, that is, the appearance frequency of the gene corresponding to said GS is low in tissue B", by examining the expression frequency of the gene corresponding to said GS in a test sample of tissue B from a patient using said GS as a probe or primer, it may be possible to identify the pathogenic gene, wherein an unusually high expression frequency of said gene being a strong indication that said GS may be the gene involved in the pathogenesis. Furthermore, by conventional methods for cloning said full-length cDNA using said GS as a probe or primer, it is possible to isolate said pathogenic gene and elucidate its characteristics.

In practice, the DNA of the present invention may be used as a probe or primer for detecting and diagnosing disease, cloning a pathogenic gene or related gene, cloning a viral gene, identifying and recognizing cell types, cloning a species-specific promoter and gene mapping.

One GS corresponds to one mRNA. It is therefore obvious that any portion of cDNA complementary to each mRNA carry the same "information for expression" as the GS. Accordingly, the DNA of the present invention is not restricted to "the DNA comprising the GS itself or portion thereof", but also includes the DNA comprising, for example, "a full-length cDNA complementary to each mRNA" and "the non-GS region of the cDNA complementary to each mRNA or a portion thereof". They can be used as a probe or primer comprising the same "expression information" as that of the GS and can be used as a probe or primer in a similar manner as a GS. For example, by using a GS or a portion thereof as a probe or primer, it is obviously possible for those skilled in the art to readily isolate "a full-length cDNA corresponding to each mRNA" or "the non-GS region of the cDNA complementary to each mRNA or a portion thereof". For example, as described hereinafter, conventional techniques such as "5' RACE", "nesting" and "inverse PCR" can be used.

An example of the method for detecting disease using the GS of the present invention will be described. As shown in Tables 1 - 219, with the method described above it is possible to detect a GS present specifically in a cDNA library constructed from each tissue by detecting and comparing the frequency of appearance of GS in each tissue. It is also possible to identify a GS corresponding to a protein which is expressed commonly in various tissues or which is expressed at low frequency. These GSs are denatured and then fixed on an appropriate filter, for example, nylon filter or nitrocellulose filter. It is

convenient to use a single filter with many GSs fixed on it. Usage of a single filter on which many denatured DNAs are fixed is well known. An example may be "the Escherichia coli Gene Mapping Membrane" (Takarashuzo, code No. 9035). It is a single nylon filter on which the cosmid contigs of genomic DNA of E. coli are fixed. It is possible to prepare a filter comprising a group of specific GSs corresponding to proteins expressed in a particular tissue, a filter comprising a group of GSs corresponding to proteins commonly expressed in various tissues, or a filter comprising a group of GSs corresponding to proteins expressed at low frequency. The single-stranded GSs fixed on these filters are then hybridized to labeled complementary DNA fragments synthesized using "random primers" prepared from template mRNA extracted from a test tissue, using four labeled nucleotides and reverse transcriptase (labeled mRNA can also be hybridized to the filters). Similarly, labeled complementary fragments synthesized using mRNA extracted from normal tissue as the template are hybridized (labeled mRNA can also be hybridized to the filters). If the profile of hybridization to a group of GSs has been categorized beforehand by comparing the hybridization profile of various pathogenic tissues to that of corresponding normal tissues, it is possible to diagnose the pathogenic condition of a particular test tissue by comparing the hybridization profile of the test tissue with that of the corresponding normal tissue and assigning that profile to a certain category. Virus infection can be detected in the same manner as in the case of other diseases.

Next, an example of the method for cloning pathogenic genes or their related genes using the GS of the present invention is described. As described above, using the filter on which denatured GSs are fixed, the GS-hybridization profile of various pathogenic tissues and that of corresponding normal tissues are compared. A considerable difference in the hybridization intensity between normal and pathogenic tissues will be an indication that the particular GS corresponds to a pathogenic gene. If a filter comprising only GSs specific for a particular tissue is applied to a sample from that particular tissue, the probability for detecting the GS with a great difference in hybridization intensity is elevated. Also a filter comprising GSs corresponding to proteins whose expression is low will facilitate the identification of the GS corresponding to the pathogenic gene by detecting an intense signal, because the hybridization signal for these GSs is usually weak. Once a GS corresponding to a pathogenic gene is found, said pathogenic gene can be cloned by established methods such as genomic Southern hybridization using said GS as a probe and/or a primer.

Furthermore, a method for cloning a full-length gene using a GS as a probe or primer is described in detail. Cloned genes isolated in the present invention are also appropriate for use in the production of proteins useful as pharmaceutical products. mRNA is extracted from tissues by conventional methods and cDNA libraries are then prepared (See Molecular Cloning, 2nd ed. Vol. 2, Section 8 New York; Cold Spring Harbor Laboratory). In this case, it is desirable to extract mRNA from tissues in which the target gene is highly expressed. One method to detect a specific gene in libraries thus prepared is, for example, to select positive clones via hybridization using a whole or partial GS as a probe. In general, since a GS is specific for a particular mRNA, hybridization can be carried out under certain stringent conditions. Probes used are at least more than 25 bases long, preferably more than 50 bases long, and more preferably more than 100 bases long.

Furthermore, if cDNA libraries, in which the cDNA for a specific gene is concentrated, are prepared, they will be preferable for selecting said specific gene. One method useful for this purpose is carried out as follows: 1) preparation of an affinity chromatographic column of resin on which the denatured GS corresponding to the specific gene is fixed; 2) application of mRNA extracted from a tissue to said column and retention of the mRNA species corresponding to the specific gene on said column; 3) elution and concentration of said retained mRNA; and finally 4) preparation of cDNA libraries using said concentrated mRNA species as the template. Another method is the selective amplification of cDNA corresponding to the specific gene by the PCR. Selective amplification of a specific gene is carried out as follows: using a partial sequence of a GS localized toward the 3' end of the specific gene as primer, cDNA is synthesized from mRNA with reverse transcriptase and 4 NTPs. To the 3' end of a single-stranded cDNA thus obtained a homopolymer such as poly-T is attached by the action of "terminal deoxyribonucleotide transferase (TdT)". In addition, using "a primer complementary to the homopolymer" and "a primer used in said reverse transcriptase reaction, or a primer whose sequence is included in the same GS but is located proximal to the 5' end", cDNA corresponding to the specific gene may be selectively amplified by the PCR [see 5'RACE (5' Rapid Amplification of cDNA ends): PNAS, Vol. 85, pp. 8998 - 9002 (1988); Nucleic Acids Res., Vol. 17, pp. 2919-2932 (1989)]. In addition, instead of the attachment of a homopolymer, there is another method comprising the following steps: 1) a single stranded anchor DNA is linked to the 3' end of a single stranded cDNA using "T4 DNA ligase"; and 2) said cDNA is amplified by the PCR using a primer complementary to said anchor DNA [Nucleic Acids Res., Vol. 19, pp. 5227-5232 (1991)]. Said primer is desirably more than 13 bases long, preferably more than 15 bases long, and more preferably more than 18

bases long. Furthermore, in order to enhance the efficiency of heat denaturation in the cycling reaction, said primer is preferably less than 50 bases long and more preferably less than 30 bases long. By linking said amplified DNA to a vector, a cDNA library concentrated with respect to the target gene is prepared.

In addition, it may be also possible to isolate a cDNA clone corresponding to the specific gene directly from the PCR products. Specifically, the PCR products are first separated by gel electrophoresis, subjected to Southern blotting analysis using the denatured GS as a probe, and examined for the presence of a band which specifically hybridizes to said GS. If a GS-hybridized band is detected, it is highly possible to isolate the cDNA clone corresponding to the specific gene by excising said band from the gel and subjecting it to direct cloning.

As described above, in order to further amplify the specific gene previously amplified by the PCR, it may be possible to perform the second PCR of the primary PCR products by replacing either or both primers previously used with a primer having the base sequence internal to said two primers (nesting) (Journal of Virology, Vol. 64, p. 864 (1990)). Nesting may be performed directly upon the products of the primary PCR. Alternatively, if a band which specifically hybridizes to the GS is detected by the Southern blotting analysis of the primary PCR products, nesting may be performed for the DNA obtained by excision of the band followed by extraction. In the case where a band which specifically hybridizes to the GS is detected by the Southern blotting analysis of nested products using the denatured GS as a probe, it is highly possible to successfully isolate the cDNA clone corresponding to the target gene by excising said band from the gel and subjecting it to direct cloning.

The isolated cDNA clone corresponding to the target gene may often correspond to the full-length mRNA, but it may be a cDNA with the 5' end deleted. In the case where the 5' end is deleted it is possible to isolate the full-length cDNA clone by conventional methods. For example, by screening a cDNA library using a probe comprising the base sequence in the 5' end region of the cloned cDNA, since the target position of said probe is shifted further toward the 5' end of the full-length cDNA than in the case of using a GS as a probe, it is possible to isolate only longer cDNA clones as the positive clone. Also by synthesizing cDNA using "a primer comprising the base sequence in the 5' end region of the cloned cDNA" with mRNA as the template followed by PCR amplification of "a single stranded cDNA having a homopolymer or anchor DNA sequence at the 5' end" and using "the primer used for previous cDNA synthesis or a primer having the sequence internal to that of said primer" and "a homopolymer or a primer complementary to anchor primer" as described above for the 5' RACE method, only the sequence toward the 5' side of the cDNA may be selectively amplified since the position of said primer is shifted further toward the 5' side of the full-length cDNA. Even if the cDNA thus obtained has a deletion at the 5' end, the population of cDNA fragments covering the full-length of the long cDNA may be obtained by repeating this procedure. It may be easy for those skilled in the art to obtain a full-length cDNA by suitably linking said cDNA fragments having overlap segments together.

Alternatively, by performing the inverse PCR (Inverse PCR: Genetics, Vol. 120, p. 621 (1988); Molecular Cloning, 2nd ed., Vol. 2, 14.12-14.13 (New York: Cold Spring Harbor Laboratory)), it may be possible to isolate a cDNA clone extending externally from the GS, that is, in the genomic DNA region. Specifically, the target DNA (genomic DNA or cDNA) is digested with restriction enzymes into fragments of about 2-3 kb and then circularized by ligating the cleaved ends. By performing the PCR for said DNA using "a set of primers which are complementary to the cDNA clone isolated using the GS or the GS as a probe or primer, and thereby making the direction of DNA synthesis mutually opposite (outward), it may be possible to amplify the DNA region extending externally from the GS. There is known a method to isolate a full-length genomic DNA of a specific gene by repeating this procedure (Nucleic Acids Res., Vol. 16, p. 8186 (1988)).

In addition, although "Taq polymerase" is conventionally used in the PCR described above, the cloning procedure may be more efficiently performed using the "LAPCR (long and accurate PCR" technique (Nature Genet., Vol. 7, p. 350-351 (1994), Nature., Vol.369, p.684-685(1994)).

Furthermore, needless to say that by linking said full-length gene thus obtained to a suitable expression vector followed by its expression in an appropriate host, it is possible to obtain the corresponding gene product (Molecular Cloning, 2nd ed.).

Next, there will be described an example of the method for identifying and recognizing cell types using the GS of the present invention. As shown in Tables 1 - 219, based on the appearance frequency of GS in each tissue and its comparison among tissues, it is possible to identify those GSs specifically present in a cDNA library constructed for each tissue. These "tissue-specific GSs" are fixed on a filter. It will be more convenient if GSs specific to each tissue are collected and fixed on a filter as a whole (e.g., a GS block specific for hepatocytes or cerebral cortex cells). As described above, to this filter are hybridized labeled complementary fragments synthesized using "random primers" prepared from mRNA extracted from test tissues or cells, "nucleotide containing 4 labeled nucleotides", and "reverse transcriptase". (Directly labeled

mRNA can also be hybridized to the filters.) Depending on the type of tissues or cells, intense hybridization signals will be observed with the GS groups specific to said tissue or cell. Furthermore, a tissue-specific promoter can be cloned by structure analysis of the 5' upstream sequence through the cloning of the corresponding gene using established methods such as genomic Southern hybridization with the "tissue-specific GS" as the probe and/or primer.

These tissue-specific promoters thus obtained are useful for gene therapy in the future.

Gene therapy in a narrow sense aims to supplement the defective protein of patients using gene technology, and in this case it is necessary to express the exogenous gene in a desired tissue in a desired quantity. For this purpose, a promoter which is known to be expressed in a specific tissue in a desired quantity (in most cases a large quantity is desired) is highly useful. Although, at present, a virus promoter is often used, it can be inactivated by endogenous modification such as methylation. Promoters provided by tissue-specific GSs will be ideal substitutes for viral promoters.

There will be described the method for chromosomal assignment of DNA corresponding to the GS of the present invention using the probe derived from the GS obtained as described above.

First, the Southern blotting method will be described.

According to this method, for example, chromosomes are isolated from a lymphoblast cell line of human normal karyotype (e.g., GM0130b), and then a monochromosomal hybrid cell is prepared by introducing each human chromosome into non-human cells, such as rodent cells, and cultured on a large scale by standard methods. Then the DNAs extracted from said hybrid cells are digested with various restriction enzymes and subjected to agarose gel electrophoresis. Then, the electrophoresed DNAs are hybridized to <sup>32</sup>P-labeled GS prepared as described above and used as the probe. By identifying the hybrid cell the DNA of which is hybridized to said probe, it is possible to identify the chromosome in which the DNA corresponding to the GS of the present invention is present. Southern hybridization test of the total human genomic DNA using each labeled GS as a probe formed a single band corresponding to the GS, indicating that the DNA of the present invention can be used as a desirable probe for human genomic DNA. It is obvious that a desirable probe for human genomic DNA can be used also as a desirable probe for human cDNA and human mRNA.

A method similarly using the PCR to determine chromosomal localization of the GS of the present invention will be described.

To prepare most appropriate primers, base sequences are selected from the sequence of the GS in question by conventional methods, for example, by using the computer software OLIGO4.0 (National Biosciences) and the oligonucleotides (20-24mer) having the selected sequences are synthesized. The preferred size of the sequence to be amplified by the PCR is from 50mer to 100mer.

Using the primers thus synthesized and the chromosomal DNA extracted from the monochromosomal hybrid cell as such as the template, amplification by the PCR is performed in a conventional manner. Resulting PCR products are subjected to non-denatured acrylamide gel electrophoresis and stained with ethidium bromide for fluorescent detection. The sizes of these PCR products are then determined.

Chromosomal assignment is confirmed when the presence of a PCR product of correct size is confirmed.

It is evident that a chromosome or chromosomes in which the DNA corresponding to a GS is localized can be identified by using these procedures. It has also become evident that the DNA of the present invention can be used as desirable primers for human genomic DNA since a single band has resulted from amplification of the total human genomic DNA by the PCR using primers designed based on each tested GS. Obviously, a desirable primer for human genomic DNA is also a desirable primer for human cDNA and human mRNA.

#### Brief Description of Figures

Fig. 1 shows the preparation of 3' Mbol cDNA library.

Fig. 2 shows the results of tests of primers. A shows the location of primers on the vector; and B shows the electrophoretic patterns of DNA fragments amplified using the primers (A). Primers used are as follows: lane 1, FW (-40)/RV (-14); lane 2, FW (-40)/RV (-36); lane 3, FW (-40)/RV (-71); lane 4, FW (-40)/RV (-29); and lane 5, FW (-47)/RV (-48). Artifacts are indicated by arrows.

Fig. 3 shows the electrophoretic pattern of PCR products using FW(-40) and RV(-14) as primers. The lane at the right end shows the electrophoretic pattern of size markers and the other lanes show the PCR products using FW (-40)/RV (-14) as primers.

Fig. 4 shows the mRNA concentration reflecting the frequency of appearance of each GS in the cDNA library: especially, Figs 4A - 4D; experimental results; Fig. 4E, photographs of colonies; and Fig. 4F,

summary.

- Fig. 5 shows the appearance frequencies for various cDNAs in the 3'-directed HepG2 cDNA library.  
 Fig. 6 shows the genetic mapping of each GS (gs) using PCR.  
 Fig. 7 shows the genetic mapping of each GS (gs) using PCR.  
 5 Fig. 8 shows the genetic mapping of each GS (gs) using PCR.  
 Fig. 9 shows the genetic mapping of each GS (gs) using PCR.  
 Fig. 10 shows the genetic mapping of each GS (gs) using PCR.  
 Fig. 11 shows the chromosomal mapping of GS001418 (gs001418) using PCR.  
 Fig. 12 shows the chromosomal mapping of GS001457 (gs001457) using PCR.  
 10 Fig. 13 shows Southern blotting of human total chromosomes using the GS as a probe.  
 Fig. 14 shows Southern blotting of human total chromosomes using the GS as a probe.  
 Fig. 15 summarizes the characteristics of hybrid cells used for Southern hybridization.  
 Fig. 16 shows Southern blotting of chromosomal DNA from the hybrid cells using GS000152 (clone s14g02) as a probe.  
 15 Fig. 17 shows Southern blotting of chromosomal DNA from the hybrid cells using GS000041 (clone s650) as a probe.  
 Fig. 18 shows Southern blotting of chromosomal DNA from the hybrid cells using GS000181 (clone hm01e01) as a probe.  
 Fig. 19 shows Southern blotting of chromosomal DNA from the hybrid cells using GS000055 (clone  
 20 c13a18) as a probe.  
 Fig. 20 shows Southern blotting of chromosomal DNA from the hybrid cells using GS000180 (clone s479) as a probe.  
 Fig. 21 shows Southern blotting of chromosomal DNA from the hybrid cells using GS000094 (clone s173) as a probe.  
 25 Fig. 22 shows Southern blotting of chromosomal DNA from the hybrid cells using junk (clone hm01g02) as a probe.  
 Fig. 23 shows the chromosomal mapping of each GS by Southern blotting. E stands for EcoRI, Ba stands for BamHI, Bg stands for BgIII and E/B stands for double cleavage with EcoRI and BamHI.  
 Fig. 24 shows the chromosomal mapping of each GS by Southern-blotting. E stands for EcoRI, Ba  
 30 stands for BamHI, Bg stands for BgIII and E/B stands for double digestion with EcoRI and BamHI.  
 Fig. 25 shows the chromosomal mapping of each GS by Southern blotting. E stands for EcoRI, Ba stands for BamHI, Bg stands for BgIII and E/B stands for double digestion with EcoRI and BamHI.  
 Fig. 26 shows the chromosomal mapping of each GS by Southern blotting. E stands for EcoRI, Ba stands for BamHI, Bg stands for BgIII and E/B stands for double digestion with EcoRI and BamHI.

#### Preferred embodiments of the invention

In the following section, there will be explained preferred embodiments of the present invention. However, the present invention will not be restricted to these preferred embodiments.

#### [Example 1]

##### Preparation of mRNA

- 45 Cytoplasmic RNA was extracted from a liver cancer cell line HepG2 (Aden., et al., Nature 282, 615-617, 1979) using standard procedures [Sambrook, J., et al., Molecular Cloning, 2nd ed. (New York: Cold Spring Harbor Laboratory), vol. 1, pp. 7.3-7.36, 1989]. Briefly, HepG2 cells grown in Dulbecco's modified Eagle medium supplemented with 10% FCS were lysed in RNA extraction buffer [0.14 M NaCl, 1.5 mM MgCl<sub>2</sub>, 10 mM Tris-HCl (pH 8.6), 0.5% NP-40, 1 mM DTT, 1000 units/ml RNase inhibitor (Pharmacia)] by using a  
 50 Vortex mixer for 30 sec and then left standing on ice for 5 min. Nuclei and other cell debris were precipitated by centrifuging at 12,000 g for 90 sec, and the supernatant was deproteinized with Proteinase K followed by phenol extraction. RNA was precipitated by isopropanol and rinsed with 70% ethanol. Finally, the poly A<sup>+</sup> fraction was collected by oligo dT column fractionation (Aviv., et al., Proc. Natl. Acad. Sci. USA 69, 1408-1412, 1972).

## [Example 2]

## Preparation of vector primer DNA and construction of cDNA libraries

5 To prepare a vector primer, pUC19 DNA amplified in JM109 cells (Yanisch-Perron, C., et al., *Gene* **33**, 103-119, 1985) was digested with PstI to completion and a poly T-tail was added with terminal transferase (Pharmacia) to a mean length of 26. This process was monitored by the incorporation of <sup>3</sup>H-deoxythymidine triphosphate [Okayama, H., et al., *Methods in Enzymology* (San Diego: Academic Press), vol. **154**, pp. 3-28, 1987]. The product was digested by HincII, and the resulting short fragments were eliminated by  
10 chromatography with Sepharose S-300. Then the T-tailed plasmid was purified by an oligo dA column and stored in 50% ethanol at a concentration of 1 µg/µl.

Fig. 1 shows the outline of the construction of the cDNA library. Two micrograms each of the cytoplasmic Poly A<sup>+</sup> RNA and the vector primer DNA were co-precipitated in 70% ethanol containing 0.3 M Na-acetate and the pellet was dissolved in 12 µl of distilled water. For the first strand synthesis, after heat  
15 denaturation at 76 °C for 10 min, 4 µl of 5 x reaction buffer [250 mM Tris-HCl (pH 8.3), 375 mM KCl, 15 mM MgCl<sub>2</sub>], 2 µl of 0.1 M DTT and 1 µl of 10 mM each of dATP, dCTP, dGTP and dTTP were added to the sample at 37 °C. The reaction was initiated by the addition of 200 units of reverse transcriptase MMLV-H-RT (BRL), and after incubation at 37 °C for 30 min, stopped by transferring the reaction tube onto ice. For the second strand synthesis, to the aforementioned reaction mixture the following was added: 92 µl of  
20 distilled water, 32 µl of 5 x E. coli reaction buffer [100 mM Tris-HCl (pH 7.5), 20 mM MgCl<sub>2</sub>, 50 mM (NH<sub>4</sub>)-<sub>2</sub>SO<sub>4</sub>, 500 mM KCl, 250 µg/ml of BSA, 750 µM βNAD], 3 µl of 10 mM each of dATP, dCTP, dGTP and dTTP, 15 units of E. coli ligase (Pharmacia), 40 units of E. coli polymerase (Pharmacia), and 1.5 units of E. Coli RNase H (Pharmacia). The reaction mixture was then incubated at 16 °C for 2 h and heated to 65 °C for 15 min. Then 20 units each of BamHI and MboI were added, and the reaction mixture was incubated at  
25 37 °C for 1 h and heated again at 65 °C for 30 min. Finally, the sample was diluted up to 1 ml with 1 x E. coli reaction buffer, and 100 units of E. coli ligase were added. The resulting mixture was incubated at 16 °C overnight. An aliquot of this mixture was used to transform competent E. coli DH5 cells (Toyobo). Transformants were selected by ampicillin resistance. The product was named "3' MboI cDNA library".

## 30 [Example 3]

## Amplification of cDNA insert by PCR

The plasmid-carrier E. coli colonies were picked into 96-well plates containing 125 µl of LB medium  
35 (Davis, R. W., et al., *Advanced Bacterial Genetics*. New York: Cold Spring Harbor Laboratory, 1980) in each well and incubated in a moist chamber at 37 °C for 24 h. A replica culture was made for every plate using a 96-pinned replica device (Sigma) and the master plates were stored at -80 °C for future use. After overnight incubation at 37 °C, 50 µl of the culture from each well of these replicas were transferred to polycarbonate 96-well plates (Techne). Bacteria were collected by centrifugation in an Omnispin H4211 rotor (Sorvall) at  
40 1500 rpm for 5 min, resuspended in 50 µl of water, covered with a layer of mineral oil and lysed at 95 °C for 30 min in a metal bath. Debris were removed by centrifugation at 3600 rpm for 30 min in the same rotor.

Five microliters of the supernatant were added to 20 µl of distilled water and kept at 95 °C for 10 min under a layer of mineral oil. Then the denatured lysate was subjected to PCR by adding 25 µl of 2 x reaction mixture [40 mM Tris-HCl (pH 8.9 at 23 °C), 3 mM MgCl<sub>2</sub>, 50 mM KCl, 200 µg gelatin/ml]  
45 containing 5 pmol each of primers, 5 nmol each of dATP, dCTP, dGTP, dTTP and 1.25 units of Taq DNA polymerase (Cetus) at 70 °C. Temperature cycling reactions were carried out immediately after addition of the reaction mixtures using a thermal cycler either for microfuge tubes (PJ1000, Perkin Elmer Cetus) or for a 96-well plate (PHC-3, Techne); 35 repeated cycles of 30 sec at 96 °C, 1 min at 55 °C, and 2 min at 72 °C without a final extension step were performed.

50 For this method, the correct choice of primers for the PCR reaction is crucial. Therefore, preliminary tests were performed using the following primers with a predicted T<sub>m</sub> of above 60 °C.

The primers tested were a pair of primers, FW(-47) and RV(-48), which are identical to the commercially available 24 mer primers, a second pair of primers, [FW(-40) and RV(-29)], which are a longer version  
55 (21 mer) of the well-tested sequencing primers, and the primers RV(-71) and RV(-14), which have a triplet sequence at the 3' terminus identical with that in FW(-40) but is in the opposite orientation (Fig. 2A).

In most of the cases where various combinations of primers were tested, short PCR artifacts appeared, besides the expected major products (Fig. 2B, arrows indicate the PCR artifacts.). These artifacts could be reduced by raising the annealing temperature, lowering the primer concentration or lowering the substrate

concentration but in all cases the yield of the products was not high enough to serve as a template for the sequencing reaction without concentration thereof.

However, since one pair of primers [SW(-40) and RV(-14)] did not yield artifacts (Fig. 3), this pair was selected for further tests, and was found to give reproducible results. Similar results were obtained with randomly selected cDNA clones. Therefore, only this pair of primers SW(-40) and RV(-14) was used as the primers of the present embodiment.

[Example 4]

#### 10 DNA sequencing

The PCR products were drop-dialyzed against TE [10 mM Tris-HCl (pH 8.0), 1 mM EDTA] on millipore filter (VS 0.025  $\mu$ m) for 90 min while stirring. Forty-eight samples are easily applied on a single filter of 150 mm diameter. Without further purification the samples were subjected to the Cycle Sequencing protocol (Applied Biosystems, 1991) using dye labeled primers with minor modifications. For dideoxycytidine sequencing reaction, 2  $\mu$ l of the dialyzed PCR reaction product (about 0.2 pmol of template DNA) were added to 3  $\mu$ l of a reaction mixture containing 0.4 pmol of FAM M13 (-21) Primer (Applied Biosystems) in 160 mM Tris-HCl (pH 8.9), 40 mM (NH<sub>4</sub>)<sub>2</sub>SO<sub>4</sub>, 10 mM MgCl<sub>2</sub>, 50  $\mu$ M dATP, 12.5  $\mu$ M dCTP, 75  $\mu$ M 7-deaza-dGTP (Boehringer Mannheim Biochemicals), and 50  $\mu$ M dTTP, 25  $\mu$ M dddCTP, 0.8 unit of Taq Polymerase (Perkin Elmer Cetus), and subjected to 15 plus 15 cycles of the reaction (95 °C 30 sec, 60 °C 1 sec, 70 °C 1 min and 95 °C 30 sec, 70 °C 1 min) according to the manufacturer's recommendation in a 96-well plate using a thermal cycler (PHC-3, Techne). The three other sequencing reactions for dideoxyguanosine, dideoxyadenosine, and dideoxythymidine were performed in parallel (with TMRA, JOE, and ROX primers respectively, supplied by Applied Biosystems) in an identical fashion, except that twice the volume of all the ingredients was added to the dideoxyguanosine and dideoxythymidine reactions. Each sample, from a set of four was cooled to 4 °C, pooled, precipitated with ethanol, resuspended in 6  $\mu$ l of a solution of formamide/50 mM EDTA (5/1 by v/v), loaded onto sequencing gel and analyzed by a DNA autosequencer (Model 373A Ver 1.0.1, Applied Biosystems).

#### 30 [Example 5]

The frequency of appearance of each GS of the cDNA library reflects mRNA population.

To confirm that our 3'-directed regional cDNA library was a non-biased representation of the mRNA population in HepG2 cells, the inserts of four cDNA clones (EF-1 $\alpha$ ,  $\alpha$ -1-antitrypsin, hnRNP core protein A1 and inter- $\alpha$ -trypsin inhibitor) from the clones redundantly obtained by random selection of cDNA were radiolabeled and used as probes in a Northern analysis of poly A<sup>+</sup> mRNA from the HepG2 cells. (The results are shown in Fig. 4A-D, and summarized in Fig. 4F.) The relative band intensity of the four mRNA species demonstrated that their relative ratios were 52, 24, 1 and 1.2, respectively (lane iii in Fig. 4F). Then the same set of probes was used for measuring the number of colonies hybridizing with each probe in the same cDNA library of 8,800 clones (Fig. 4E).

The clonal frequencies were 307, 128, 7 and 9, or in ratio, 44, 17, 1 and 1.3, respectively (lane iv in Fig. 4F). These two estimates agreed, showing that the cDNA library used is a non-biased representation of the mRNA population. The ratio was practically unchanged when different preparations of mRNA from the same cell were tested.

Fig. 4 shows the proportionality of the composition of the 3'-directed cDNA library and of the mRNA. Fig. 4A, 2  $\mu$ g of poly A<sup>+</sup> RNA from HepG2 cells was electrophoresed in lanes 1-4 of a formamide agarose gel containing ethidium bromide (5  $\mu$ g/ml) and then exposed to UV. Lane 5 is the RNA ladder (BRL) used as size markers (kb). In Fig. 4B, the filter was northern blotted using the following <sup>32</sup>P-labeled 3'-specific cDNA probes: Elongation factor-1 $\alpha$  (lane 1),  $\alpha$ -1-antitrypsin (lane 2), HnRNP core protein A1 (lane 3), inter- $\alpha$ -trypsin inhibitor (lane 4). In Fig. 4C, one pmol each of the non-labeled cDNA fragments [EF-1 $\alpha$  (lane 1),  $\alpha$ -1-antitrypsin (lane 2), HnRNP core A1 (lane 3), inter- $\alpha$ -trypsin inhibitor (lane 4), were electrophoresed in a 2% agarose gel, then photographed. Fig. 4D is a Southern analysis of the blotted filter from Fig. 4C, using the same set of radioactive probes. Lane 5 shows the migration pattern of the reference 1 kb ladder (BRL). Hard copies of these screen images were taken at 8 h for b, and 1 h for d. The radioactivity in each band was counted directly in a scinti-scanner ( $\beta$ -603; Betagen) and registered in (i) and (ii) in Fig. 4F. The observed band intensities were corrected based on the band intensities in Fig. 4D (ii in Fig. 4F), and normalized relative to the value of probe 3 (HnRNP core A1, lane iii in Fig. 4F) as 1 (iii in Fig. 4F). These values represent the relative content of each mRNA species in the original mRNA preparation. Fig. 4E



shows the results of colony hybridization of the membranes carrying 8,800 colonies of the 3'-directed cDNA library using the same set of the four radioactive probes. Positive colonies were counted and registered (iv in Fig. 4F), then normalized with the value of HnRNP core protein A1 as 1. The numbers in B, D and E in Fig. 4 represent the probe No. in Fig. 4F. Fig. 4F shows a remarkable agreement between the values of lanes (iii) and (v).

[Example 6]

#### Population study of the cDNA library

To analyze further the composition of the cDNA library, 7 and 10 clones were selected from the redundant (group I) and solitary (group II) sequence groups, respectively, and these inserts were used as radiolabeled probes for colony hybridization (Fig. 6). The frequencies of the colonies that hybridized with group I probes were roughly identical to those that were randomly picked and sequenced. These frequencies were about 3.5%-0.1%. Nearly 52% of the cDNA library population consisted of the redundant sequence group containing 173 species. When 8 probes from group II were tested, 18 positive colonies were identified among 26,400 colonies screened, giving an average frequency of 0.007%. Two probes did not hybridize with any of the 26,400 colonies, resulting in the average frequency of <0.004%. Thus, the average frequency of the 10 probes in group II was several orders of magnitude less than the lowest of group I.

The results are summarized in Fig. 5, showing the appearance frequencies of various DNA species in the 3'-directed HepG2 cDNA library. In Fig. 5, seven cDNA probes (a15 through tb042) were selected from the 162 identified genes in the redundant group (group I), and ten (s155 through s632) were randomly chosen from the solitary group (group II). In columns A, B and C, each one of the insert DNAs was radiolabeled and used as a probe for colony hybridization tests of 982 (A), 8,800 (B) or 26,400 colonies (C). NT indicates "not tested". The DDBJ entry names of the 17 clones listed in this table are HUM000A15, HUM000C321, HUM00TB038, HUMHM01B02, HUM0C13A04, HUMHM02D02, HUM00TB042, HUM000S155, HUM000S159, HUM000S639, HUM000S635, HUM000S170, HUM000S154, HUM000S167, HUM000S645, HUM000S647, and HUM000S632.

[Example 7]

#### Analyses of sequencing errors

All the sequence data presented in this specification were obtained by repeated cycles of enzymatic amplification of the plasmid inserts, followed by cycle sequencing with Taq polymerase. Sequences of 60 clones that showed data bank matches were examined for discrepancies from the data bank entries. It was found that the accuracy in the region 1-100 bp distant from the cloning site was 98.7%, indicating that the primers or probes designed with the sequence in this region could be obtained practically without any erroneous sequences or even if they contain any errors, they are functionally without problems.

[Example 8]

#### Mapping of GS by PCR

(cDNA sequence)

cDNA library was constructed from mRNA of DMSO treated HL60 cells. The methods for construction of the 3'-directed cDNA library and for sequence analysis of the library components are the same as described in Examples 1-4.

(PCR primer)

Primer design was performed by using the computer software OLIGO 4.0 (National Biosciences) which eliminates possible formation of inter- or intra-molecular secondary structures. In addition to the primer design, transfer of oligonucleotide sequences to the local database and synthesizer were semiautomated using a Macintosh computer linked with a network. DNA oligomers were synthesized on an automated DNA synthesizer (Model 394, Applied Biosystems) on a 40 nmol scale. The synthesized oligomers were used as

PCR primers without further purification.

(Preparation of Genomic DNA)

- 5 The human genomic DNA was extracted from the normal karyotype lymphoblastoid cell line GM0130b. Mouse and Chinese hamster genomic DNAs were purchased from Clontech. Monochromosomal hybrid cells utilized for mapping panel were commonly used ones which have been described previously. Briefly, chromosomes 3, 4, 9, 11, 12, 13, 15, 22 and Y were carried in human-Chinese hamster monochromosomal hybrid cells, and chromosomes 1, 2, 5, 6, 7, 8, 10, 11, 12, 14, 15, 16, 17, 18, 19, 20, 21 and X were carried  
10 in the human-mouse monochromosomal hybrid cells A9 series. The integrity of the hybrid cells were monitored by *in situ* hybridization.

(Amplification by Polymerase Chain Reaction)

- 15 PCR was performed according to standard protocols (Saiki, R. K., et al., Science 230, 1350-1354, 1985), using 10 pmol of each primer on a whole 20  $\mu$ l scale reaction, with 35 thermal cycles of 30 sec at 94 °C, 60 sec at an annealing temperature, and 90 sec at 72 °C, using a Perkin-Elmer 9600 thermal cycler. Annealing temperature was determined according to the "optional annealing temperature" estimated by the Program OLIGO.

- 20 (Analysis of the PCR Products)

- The PCR products were run on an 8% polyacrylamide non-denatured gel (Acrylamide:Bis-acrylamide = 19:1, 1 mm thick) at 300 V for 1 h, followed by staining in 90 mM Tris-borate, 2 mM EDTA buffer solution  
25 containing 0.25  $\mu$ g/ml ethidium bromide for 15 min. The size of the amplification products were determined relative to the 10 bp DNA ladder (BRL). Detection of fluorescence was performed by using a laser fluorescent image analyzer (FM-BIO, Hitachi Software Engineering). The image data were transferred to a computer for analysis.

- 30 (Results of Analysis of the PCR Products)

- Among various species of 3'-directed cDNA-GSs obtained from granulocytoid cells, 195 novel GSs which did not match the sequences deposited in Genbank Release 76 were selected and used for designing primers for the PCR. The PCR was performed with these primers using the total human genomic  
35 DNA as the template.

- Among the 195 primer pairs, 191 (98%) yielded products whose size matched those expected within 5 nt. The results are summarized in Figs. 6 - 10 whose figure legends are as follows: GS, gene signature; CN, clone name; Chromosomal position, chromosome numbers to which GSs were mapped; Sequence of primers, DNA sequences of primers (Sense, sense strand; anti-sense, anti-sense strand); AT, annealing  
40 temperature; HO, Observed size of PCR products with total human genomic DNA (nt); HE, Expected size of PCR products with total human genomic DNA (nt); MO, Observed size of PCR products with mouse genomic DNA (nt); CO, Observed size of PCR products with Chinese hamster genomic DNA (nt); G, Number of "hits" of GS in the granulocytoid (DMSO treated HL60) cDNA library after analyzing altogether 1000 clones; T, Total number of "hits" of the GS after analyzing altogether 3000 clones from the three  
45 cDNA libraries of HL60 with and without induction by DMSO or TPA. Question marks (" ? ") indicate that the PCR products did not yield a clear band.

- "M" indicates that the PCR products yielded a band which was indistinguishable from the band observed after the reaction using mouse DNA as the template. Similarly, "C" indicates that the PCR products yielded a band which was indistinguishable from the band after the reaction using Chinese  
50 hamster DNA as the template.

- The overall rate of success of the PCR was 191/195 (98%), although GSs were randomly selected from the cDNA sequences, indicating that the quality of the cDNA library used in this work was reliable, and that the sequence analyses and primer designs were performed appropriately. Thus, the possible chances of failure of the PCR caused by presence of an intron(s) in the relevant cDNA sequences is negligible in  
55 working with the GS, as introns virtually do not lie in the poly A proximal 3'-region of vertebrate genes (Wilcox et al., Nucleic Acids Res. 19, 1837-1843, 1991). This is a big advantage compared to the use of partial fragmented cDNA sequences obtained from randomly primed cDNA libraries (Adams et al., Science 252, 1651-1656, 1991) or from 5'-directed cDNA libraries.

## (Chromosomal assignments of GS)

The 191 primer pairs that yielded PCR products from total human DNA were used for chromosomal assignments of the GSs with the monochromosomal hybrid cell panel. At least 119 GSs were assigned to a single chromosome. As an example, GS001418, shown in Fig. 11, was assigned to chromosome number 3. With some clones, extra products were obtained, some of which were assigned to the same chromosome, whereas others to different chromosomes. An example, GS001457, is shown in Fig. 12. Sixty-two (33%) clones yielded the expected PCR products with two or more different chromosomes. Thirty-five cases (18%) yielded PCR products whose size were indistinguishable from background rodent genomic DNA. Among these, 21 GSs produced products indistinguishable from mouse and Chinese hamster DNA. Ten GSs yielded no expected PCR products with the monochromosomal cell panel DNA although the expected PCR products from total human genomic DNA were observed. The 10 cases probably arose from a small deletion in the hybrid cells. Five clones obtained from HepG2 cDNA library have been analyzed also by Southern blot analysis. Four out of the 5 GSs (GS000053, GS000120, GS000271 and GS000279) gave consistent results with those obtained by the PCR. One GS (GS000228), which was uncertainly assigned to chromosome Y because of the weak signal detected by the Southern blot method, was assigned to chromosome 11 by PCR.

## [Example 9]

## Mapping of GS by Southern blot method

## (Cell lines)

Total human genomic DNA was isolated from the human normal karyotype lymphoblastoid cell line GM0130b. Monochromosomal hybrid cells used as the mapping panel are shown in Fig. 15. Hybrid A9(neo-x)-y cells as described by Koi, et al. (Jpn. J. Cancer Res. 80, 413-418, 1989) were donated by Dr. M. Oshimura, Faculty of Medicine, Tottori University, passaged 3 times and frozen for storage. The loss or rearrangements of chromosomes could have occurred during this period. The GM series was obtained from the Mutant Cell Repository, National Institute of General Medical Science (NIGMS) (Camden, NJ). To confirm that human chromosomes remained intact in the hybrid cells after storage in liquid nitrogen, metaphase spreads of the hybrid cells were monitored by chromosome staining based on *in situ* hybridization using biotinylated total human DNA as the probe (Durnam, D. M., et al., Somatic cell Mol. Genet. 11, 571-577, 1985). Intact, as well as translocated or fragmented human chromosomes were easily detected by this means. In a hybrid cell mapping panel, chromosomes 11, 12 and 15 were represented by the hybrid cell lines A9(neo-11)-1, A9(neo-12)-4 and A9(neo-15)-2, respectively, and in another panel, they were represented by the hybrid cell lines GM10927A, GM10868 and GM11418, respectively.

## (Isolation of genomic DNA and Southern blotting)

High molecular weight DNA was extracted from cells using sodium dodecyl sulfate (SDS) and Proteinase K, followed by phenol-chloroform extraction and ethanol precipitation. DNAs were digested overnight with a combination of two restriction enzymes including EcoRI, BamHI and BglII. About 5 µg of each digest was electrophoresed in an 0.8% agarose gel, then transferred to Hybond N<sup>+</sup> membrane (Amersham) with 0.4 N NaOH. The membrane was rinsed in 2 x SSC and stored at 4 °C for subsequent use.

Clones containing a novel sequence and having more than 150 bp were selected as probes. The cDNA inserts of the clones were amplified by the PCR. The PCR products were isolated by electrophoresis through a 2% low-melting temperature agarose gel (Nusieve : SeaPlaque, 3 : 1), followed by excision. The gel was removed by melting at 65 °C and digesting with  $\beta$ -Agarose I (Bio Labs) at 40 °C for 1 h. The probes were labeled with [ $\alpha$ -<sup>32</sup>P]dCTP by random priming using a commercial kit (Amersham). Hybridization proceeded at 65 °C in a high salt buffer containing 6xSSC, 1x Denhardt's solution and 0.5% SDS, in the presence of 0.1 mg/ml of sonicated, denatured salmon sperm DNA. The membranes were washed in 2xSSC, 0.1% SDS at 65 °C for 30 min, then twice for 30 min in 0.1xSSC, 0.1% SDS at 65 °C, and analyzed using a Fuji BAS-2000 imaging analyzer.

# <Analyses with Genomic DNA>

Among the HepG2 3'-directed cDNA libraries described in Examples 1 and 2, 160 novel clones were selected and used as probes for Southern blots.

5 Total human genomic DNA was isolated from a cell line GM0130b that has a normal karyotype, and digested with the restriction enzymes, EcoRI, BamHI and BglII alone or in combination. The GS clones used as probes were the 3'-directed cDNAs. Each of these cDNAs covers a region between the poly(A) site and the nearest MboI site (GATC) (Okubo, K., et al., Nature Genetics 2, 173-179, 1992) and thus do not have restriction sites for BamHI or BglII. In addition, because the average size of GS is 270 bp, the chances of  
10 having an EcoRI site in the cDNA moiety were not high. In fact, only 7 clones out of the 160 analyzed had an EcoRI restriction site.

Membranes blotted with digested human genomic DNA were hybridized with radio-labeled GS probes and washed at high stringency. Since the 3'-terminal region of cDNA has, in general, a unique sequence which differs from that of protein encoding regions which tend to have conserved motifs, cross hybridization  
15 with unrelated cDNA sequences will not occur under such stringency. Examples of the results of hybridization are shown in Figs. 13 and 14. Clones s503 and s632 (Figs. 13a and 13b; junk) respectively represent unique single band producers. As shown below, 67 clones belonged to this class. The positions of the GS sequence relative to the restriction sites were inferred from the band patterns. Clone s311 (Fig. 13c; GS000092) showed a single band with EcoRI -as well as (EcoRI + BamHI)-digested DNA, but two bands of  
20 different sizes in other double digests. The double digestion thus helped resolve multiple GSs. Similar results were obtained with clone c13a08 (Fig. 13d; GS000055), in which there were 2 bands with EcoRI- or (EcoRI + BamHI)-digested DNAs, and 4 when digested with (EcoRI + BglII) or (BamHI + BglII). On the other hand, 4 hybridization bands appeared with clone s479 with EcoRI alone, but the number of bands decreased with (EcoRI + BglII) and (BamHI + BglII) (Fig. 14e; GS000180). These results indicate that  
25 genomic DNAs should be digested in various ways to reveal the maximum number of hybridizing fragments. The results of the analysis showed that 41, 10, 7 and 19 clones contained 2, 3, 4 and 5 or more bands, respectively. Clones s14f01 and tw1-46 (Figs. 14f and 14g; GS000407 and junk, respectively) contained at least 10 bands in each lane. Since the EcoRI restriction site is not present in the two GS sequences, the multiplicity of bands is likely to represent the multiple copy number of these genes. Clone  
30 kmb07 moved as a smear (Fig. 14h; junk), even after intensive high stringency washes, suggesting that this probe has a repetitious sequence which has not been hitherto identified.

# <Chromosomal assignments>

35 A set of monochromosomal hybrid cells carrying a single human chromosome in a background of rodent chromosome was collected (Fig. 15). Thirteen cell lines were microcell hybrids established by Koi et al. (Koi, M., et al., Jpn. J. Cancer Res. 80, 413-418, 1989) and the others were obtained from NIGMS. The results of monitoring the human chromosomes in these cell lines by *in situ* hybridization using biotinylated total human DNA are also presented in Fig. 15.

40 The GSs were assigned to chromosomes using hybrid cell mapping panels. Three types of membranes were prepared, each having DNAs prepared from hybrid cells, and digested with EcoRI, (EcoRI + BamHI), or (BamHI + BglII). Among these three types of membranes, the one which should have yielded the maximum number of bands was used for each GS probe, according to the results of total genomic Southern blots. Examples of hybridization results are shown in Figs. 16 - 22. The numeral on each lane represents the  
45 human chromosome numbers which is contained in the hybrid cell, and H stands for the total human chromosomes. Clone s14g02 (GS000152; Fig. 16) that showed a single hybridization band with the total human DNA digested with EcoRI (lane H), showed the corresponding band only with the hybrid cell line containing human chromosome 4. Thus, this GS lies in chromosome 4.

The clone s650 (GS000041; Fig. 17) was assigned to chromosome 12 which showed a characteristic  
50 7.5kb band in the presence of an (EcoRI + BamHI)-digested membrane. However, with an EcoRI digested DNA, the clone could not be assigned, as the human-specific and the cross-reacting rodent DNA fragments overlapped. The single, but shorter fragment band (1.3kb) which appeared in lanes 3, 4, 9, 13 and 22 represents the homologous DNA sequence in Chinese hamster, and the 3.3kb band in other lanes represents the homologous DNA in the mouse.

55 Clone hm01e01 (GS000181; Fig. 18) exhibited two fragments when hybridized to total human DNA treated with EcoRI alone, and these corresponding bands appeared in lanes 1 and 2. Thus, the two members of this gene family are located on two chromosomes.

Fig. 19 shows that clone c13a08 (GS000055) exhibited 4 bands when hybridized to (BamHI + BglII)- or (EcoRI + BglII)-digested total human DNA, although only 2 bands appeared with EcoRI- or (EcoRI + BamHI)-digested human DNA. Therefore, the (BamHI + BglII)-digested DNA panel was used for this clone. Two bands (12.3kb and 7.5kb) appeared in lane 7, a 5.2kb band in lane 2, and a 3.2kb band in lane 17. Two bands (6.0kb and 3.8kb) that cross-reacted with Chinese hamster DNA appeared in lanes 3, 4, 9, 13 and 22, and a single band (3.5kb) that cross-reacted with mouse DNA appeared in other lanes.

Clone s479 (GS000180; Fig. 20) showed 4 EcoRI fragments with total human DNA. The hybridization to an EcoRI-digested DNA panel yielded in bands of 10.5kb in lanes 7 and 19, 8.5kb in lane 8, 7.8kb in lanes 11 and 12, and 3.5kb in lane 11. Thus, the human specific genes are dispersed among chromosomes 7, 8, 11, 12 and 19, among which the 10.5 and 7.8kb bands in the total DNA both consist of two overlapping fragments. As shown in lane H, the intensity of these overlapping fragments was higher than normal. The 3.5kb band in lane H, as well as in lane 11 was also intense, suggesting that it also represents overlapping fragments.

Clone s173 (GS000094) exhibited 5 bands in EcoRI-cleaved total DNA (Fig. 21). Four corresponding fragments included a 4.5kb fragment in lane 1. Another 4.5kb band was observed in lane 4, indicating that the corresponding band in lane H overlapped. In addition, an intense 3.1kb band was observed in lane 17.

Clone hm01g02 (junk; Fig. 22) exhibited many bands with total DNA, and with those from monochromosomal hybrids. This clone must represent a multiple and closely related family of genes. It also contains a sequence conserved in homologous rodent genes which also give rise to multiple bands. Since most of the human specific and rodent bands overlapped, the chromosomes could not be assigned. Other combinations of restriction enzymes did not resolve the overlap.

The results of the total genomic DNA analyses and the chromosome assignments of 160 GSs are summarized in Figs. 23 - 26. Through total genomic DNA analyses using 4 differently digested human DNAs, 67 clones were categorized into a single band group, 41 in a two band group, 10 in a three band group, 7 in a four band group and 19 in a group that yielded five or more bands. Nine clones did not show any hybridization band under fixed conditions.

Assignment of two band clones showed that the two genes lie in different chromosomes in 15 of them, whereas the gene represented by clone s317 originated from the same chromosome. The three band clones s308 (GS000412) and s401 (GS000224) showed that two of the fragments lie on the same chromosome, and clone hm05g02 (GS000209) and s17a10 (GS000294) showed bands in different chromosomes. Clones displaying four or more bands showed a relatively dispersed distribution among chromosomes. "junk" in Example 9 is the DNA segment cloned by the same method used for GS but is not numbered.

#### [Example 10 Cloning of gene using GS]

[10A. Cloning of a full length cDNA encoding a human ribosomal protein, homologue of yeast S28. Cloning of the full length cDNA by PCR using a primer comprising a partial sequence of a GS(1)]

Using a primer (5'-TGAAAATTTATTACTACAGTGTTCACCA-3' (SEQ ID NO:7839)) that is a partial sequence of a DNA which is substantially the same as the complementary strand of HUMGS00500 and a primer (5'-TAATACGACTCACTATAGGG-3' (SEQ ID NO: 7840)) complementary to the vector (pSPORT) sequence that is located external to the 5' end of the cDNA, HepG2 cDNA library was amplified by the PCR and a full length cDNA clone encoding a human ribosomal protein, a homologue of yeast ribosomal protein S28 was isolated. (Hori et al., Nucl. Acids Res. 21: 4394, 1993).

[10B. A human ribosomal protein homologous to rat L9 ribosomal protein-Cloning of the full length cDNA by PCR using a primer comprising a partial sequence of a GS(2)]

Using a primer 5'-CTTCTTTCTGTAGCCAGGTAAGTCT-3' (SEQ ID NO: 7841) that is a partial sequence of a DNA which is substantially the same as the complementary strand of HUMGS00418 and a primer (SEQ ID NO: 7840) complementary to the vector (pSPORT) sequence that is located external to the 5' end of the cDNA, a full length cDNA clone encoding a human ribosomal protein homologous to rat L9 was isolated (Hori et al., Nucl. Acids Res. 21:4395, 1993).

[10C. A human protein homologous to bovine phosphatidylethanolamine-binding protein. Cloning of the full length cDNA by hybridization using a probe comprising a partial sequence of a GS]

By hybridization with the probe,

5'-GATCGTTCCTTCATGGGGGTAAGAAAAGCTGGTCTGGAGTTGCTGAATG

TTGCATTAATTGTCCTGTTTGCTTGTAGTTGAATAAAAAATAGAAACCTGAAT

GAAGGAAA-3' (SEQ ID NO:7838),

that comprises a partial sequence of HUMGS00421, a full length cDNA clone encoding a human protein homologous to bovine phosphatidylethanolamine-binding protein was isolated (Hori et al., Gene 140:293, 1994).

[10D. Human mpl-ligand. Cloning of a cDNA coding for the human mpl-ligand using a GS]

This embodiment employs the 5' SLIC (single ligation to single stranded cDNA) method which is an improved version of the 5'RACE (rapid amplification of cDNA ends) method, and is described in Nucleic Acids Res., 19, 5227-5232 (1991).

#### ① Reverse transcription of cDNA and attachment of anchor

The template was prepared using the reagents of the 5'-Amplifinder™ Kit (Toyobo, Inc.) in accordance with the protocol included therewith. Specifically, 2μg of human fetal liver poly A<sup>+</sup>RNA (Clontech Laboratories, Inc.) and 10 pmol of the primer PA-6, a primer corresponding to the 3' end of the gene signature (GS) sequence HUMGS02342 and consisting of the sequence 5'-TTTTCGGCGCTCCCATTTATTCCTT-3' (SEQ ID NO: 7842), were mixed together and then denatured by heating the mixture at 65 °C for 5 min. The cDNA was synthesized by combining the denatured sample with AMW reverse transcriptase, RNase inhibitor, dNTPs, and a reaction buffer, and then heating the resultant mixture at 52 °C for 30 min. EDTA was then added to the mixture to stop the reaction. Thereafter, the RNA was hydrolyzed by adding NaOH to the reaction mixture and heating the resultant mixture at 65 °C for 30 min. The mixture was then neutralized with acetic acid. A suspension of glass beads (GENO-BIND™) and NaI were added to the neutralized solution and the cDNA was adsorbed onto the beads. The cDNA, adsorbed onto the beads, was washed with an aqueous solution of 80% EtOH, and then eluted in 50 μl of distilled water. Glycogen was added to the solution of purified cDNA, and the cDNA was precipitated with EtOH and resuspended in 6 μl of distilled water. The resultant suspension (2.5 μl) was added to a solution containing 4 pmol of AmpliFINDER Anchor (5'-CACGAATTCACATATCGATTCTGGAACCTTCAGAGG NH<sub>2</sub>-3') (SEQ ID NO: 7843) provided with the Kit, T4 RNA ligase, and a ligation (reaction) buffer. The reaction mixture was incubated at room temperature overnight, and the AmpliFINDER Anchor primer in the reaction mixture was thereby ligated to the 3' end of the cDNA. The ligated product was then used as a template for the subsequent PCR.

#### ② Amplification by PCR

The primary PCR was carried out using the template produced in the procedure described above (①), the Anchor primer, 5'-CTGGTTCGGCCCCACCTCTGAAGGTTCCAGAATCGATAG-3' (SEQ ID NO: 7846) and the PA-5 primer consisting of the sequence 5'-CTCGCTCGCCCATCCTTATACAGGCTCAGTTTTGTCT-3' (SEQ ID NO: 7844). Specifically, 1 μl of the template was mixed with Taq DNA polymerase (Takara Shuzo Inc., Code No. R001A), dNTPs, a PCR buffer, and 10 pmol each of the PA-5 primer and Anchor primer. The resultant reaction mixture was diluted with distilled water to a final volume of 50 μl and the PCR was performed in a DNA Thermal Cycler 480 (Perkin Elmer Cetus Corp.). The reaction mixture was subjected to 40 cycles of the PCR, wherein each cycle consisted of incubating the sample in sequence at 94 °C for 1 min, 63 °C for 1 min, and 72 °C for 3 min and, in the last PCR cycle, at 72 °C for an additional 8 min. The products of the PCR were resolved by electrophoresis in a 1% agarose gel and a broad band of

approximately 800 bp in length, representing a product of the PCR, was detected. The detected band was excised from the agarose gel and the DNA contained therein was recovered using a Sephaglas Bandprep Kit™ (Pharmacia Corp.) in accordance with the protocol included therewith. Specifically, the gel was dissolved in a solution of Nal and the resultant mixture was heated at 60 °C for 10 min. Sephaglas™ BP was added to the gel mixture and the DNA was adsorbed onto the glass beads contained therein. The glass beads, containing the adsorbed DNA, were then washed three times with a Wash Buffer provided with the Kit and eluted in 30 µl of TE buffer (10 mM Tris-HCl pH 8.0, 1mM EDTA).

One µl of the eluted DNA was used as a template in a secondary PCR. In order to enhance the specificity of the secondary PCR, the reaction was performed with PA-4 primer which consisted of the sequence 5'-CTCGCTCGCCCATGTATAGGGACAGCATTTCTGAGAG-3' (SEQ ID NO: 7845) and was positioned within the template sequence internal to the PA-5 primer and the Anchor primer. Specifically, 1 µl of the template was mixed with 2.5 units of Taq DNA polymerase (Takara Shuzo Inc., Code No. R001A), dNTPs, a PCR buffer, and 10 pmol each of the PA-4 primer and Anchor primer. The resultant reaction mixture was diluted with distilled water to a final volume of 50 µl preheated at 94 °C for 6 min, and the secondary PCR was then performed under the same conditions described above (①) for the primary PCR. The products of the secondary PCR were resolved by electrophoresis in a 1% agarose gel and a broad band of approximately 800 bp in length, representing a product of the PCR, was detected. The detected band was excised from the agarose gel and the DNA contained therein was recovered and purified under the same conditions as described above (①) for the primary PCR.

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### ③ Subcloning into plasmid vector

The purified DNA product of the secondary PCR was subcloned into the plasmid vector pUC18 (pharmacia Corp.), using a SureClone™ Ligation Kit (Pharmacia Corp.) in accordance with the protocol included therewith. Specifically, the purified DNA was added to a solution containing Klenow polymerase, polynucleotide kinase and a reaction buffer, mixed and heated at 37 °C for 30 min in order to create blunt-ended termini and to phosphorylate the 5' terminus of the DNA molecules contained in the reaction mixture. The blunt-ended and phosphorylated DNA was combined with a solution containing 50 ng of a dephosphorylated and Sma I-cleaved pUC18 vector provided with the Ligation Kit, T4 DNA ligase, DTT and a ligation reaction buffer, and the resultant mixture was warmed at 16 °C for 3 hr. One sixth volume of the reaction solution was employed to transform E. coli competent cells using standard methods. Specifically frozen E. coli competent cells (Wako Pure Chemical Industries, Ltd.) were thawed and mixed with the ligated DNA. The resultant mixture was incubated on ice for 20 min, heat-treated at 42 °C for 45 sec, and then incubated on ice for 2 min. A medium [Hi-Competence Broth (Wako Pure Chemical Industries, Ltd.)] was added to the mixture containing the transformed E. coli cells. The mixture was incubated for 37 °C for 1 hr and then spread onto agar plates containing 100 µg/ml Ampicillin, 40 µg/ml X-Gal (6-bromo-4-chloro-3-indolyl-β-D-galactoside), 0.1 mM IPTG (isopropyl-β-D-thiogalactopyranoside) and cultured overnight at 37 °C. White colonies were selected from the colonies which consequently appeared on the agar plates and analyzed by the PCR to determine the presence or absence of the DNA insert. Specifically, a sample of a selected colony was picked with a sterilized toothpick and used to inoculate a 50 µl reaction solution containing 1 unit of Taq DNA polymerase, dNTPs, PCR buffer, 200 µM each of the M13 P4-22 primer consisting of the sequence 5'-CCAGGGTTTCCAGTCACGAC-3' (SEQ ID No: 7847) and M13 P5-22 primer consisting of the sequence 5'-TCACACAGGAAACAGCTATGAC-3' (SEQ ID No: 7848), wherein both primers are comprised of sequences complementary to the pUC18 vector. The resultant mixture was heated at 94 °C for 6 min and then subjected to 30 cycles of the PCR wherein each cycle consisted of incubating the sample in sequence, at 94 °C for 1 min, 55 °C for 1 min, and 72 °C for 2 min. The amplified insert was detected by electrophoresis of the PCR products on an agarose gel and thereby the clone pR02342-2, containing an insert, was selected.

### 50 ④ Sequencing of cDNA

The plasmid DNA was prepared using the QIAprep-Spin Kit (Funakoshi, Ltd.) in accordance with the standard alkali-SDS protocol included therewith. Specifically, E. coli cells transformed with the DNA of clone pR02342-2 were cultured overnight in Luria Broth medium containing 100 µg/ml Ampicillin. The cultured cells were then pelleted by centrifugation and resuspended in P1 solution provided in the Kit. The resultant cell suspension was mixed with the P2 alkali solution of the Kit, incubated at room temperature for 5 min, neutralized with N3 solution of the Kit, incubated on ice for an additional 5 min and then centrifuged. The supernatant obtained from the centrifuged solution was applied to a QIAprep-Spin column. The Spin column

was then washed in sequence with PB and then PE solution of the Kit and the DNA was eluted from the column with TE buffer. Sequencing of the eluted DNA was then carried out using the sequencing kit PRISM™ Terminator Mix (Applied Biosystem Corp). Approximately 1 µg of the purified DNA was mixed with a solution containing 3.3 pmol of either the M13 P4-22 primer or M13 P5-22 primer and 9.5 µl of PRISM™ Terminator Mix. The M13 P4-22 and M13 P5-22 primer were used to sequence both strands of the DNA insert of clone pR02342-2. The resultant mixture was diluted to a final volume of 20 µl with distilled water and subjected to 25 cycles of the PCR wherein each cycle consisted of incubating the sample in sequence at 96 °C for 30 sec, 50 °C for 15 sec, and 60 °C for 4 min. The excess primers and fluorescent dye present in the reaction mixture were removed by gel filtration using a MicroSpin™ S-200 HR column (Pharmacia Corp.) and the DNA products of the sequencing reaction were precipitated with EtOH. The precipitated DNA was resuspended, sequenced using an automated sequencer, "Model 373A" (Applied Biosystem Corp.), and thereafter analyzed to determine the nucleotide sequence.

The analysis of the nucleotide sequence revealed that the insert of clone pR02342-2, including the PA-4 primer, was 608 bp in length. The sequence of this insert was subjected to a search for homologous sequences entered in the Gen Bank data base, and a 100% match was found to a sequence in the cDNA which encodes the human mpl-ligand (Accession No. L 33410, Nature 369, 533-538, 1994). Further comparison of the insert of clone pR02342-2 with the cDNA sequence of the human mpl-ligand revealed that the cloned insert contained 81 bp of the 3' coding region of open reading frame. In addition, the insert of clone pR02342-2 contained an additional sequence extending beyond the 3' end of the human mpl-ligand cDNA sequence registered under Gen Bank Accession No. L 33410. These findings suggest that, using the GS HUMGS02342, the inventors of the present invention succeeded in cloning a cDNA clone pR02342-2, which could possibly have a different and more desirable property for expression than the human mpl-ligand cDNA represented by the sequence registered under Gen Bank Accession No. L 33410.

#### 25 ⑤ Cloning of the full-length cDNA encoding the human mpl-ligand

In order to find an optimal PCR primer, an appropriate computer program is used to search the sequence downstream of the coding region of the human mpl-ligand (clone pR02342-2) and thereby a primer PA-7 is designed and synthesized. A PCR similar to that described above in ② is performed using the template produced by the procedure described above in ①, the Anchor primer, and the PA-7 primer. Specifically, 1 µl of the template is mixed with 2.5 units of Taq DNA polymerase (Takara Shuzo Inc., Code No. R001A), dNTPs, a PCR buffer, and 10 pmol each of the PA-7 primer and Anchor primer. The resultant reaction mixture is diluted with distilled water to a final volume of 50 µl and the PCR is performed in a DNA Thermal Cycler 480 (Perkin Elmer Cetus Corp.) under conditions similar to that described above in ②. The products of the PCR are then resolved by electrophoresis on a 1% agarose gel and a band greater than 1300 bp in length, representing a product of the PCR, is recovered and cloned into a suitable vector in a manner similar to that described in ③. The cloned DNA is sequenced in a manner similar to that described in ④. The sequence is then compared to that of the human mpl-ligand cDNA registered under Gen Bank Accession No. L 33410 to confirm the presence of the full-length open reading frame.

Alternatively, using the Takara La PCR Kit (Takara Shuzo Inc., Code No. RR011) in accordance with the protocol included therewith, performing the 5'RACE procedure using primers similar to those described above in ②, a cDNA of approximately 2 Kb in length, corresponding to the human mpl-ligand, was isolated.

The tables of appearance frequencies for all GSs related to the present invention are followed by "Sequence Listing" for these GSs, wherein HUMGS numbers after the heading 'clone' represent GS numbers. In the sequence table, N in the base sequence stands for "A or C or G or T or U". However, since nucleic acids in the Sequence Listing are DNAs, "T or U" stands for T in this case.

By the present invention, it has become possible to provide DNA molecules which carry "the information for expression" in various cells and can be used for detecting and diagnosing the cellular abnormalities, recognizing and identifying cells and further efficiently cloning genes which are expressed in a tissue-specific manner, and furthermore cloned DNA molecules which can be used for the production of proteins useful as pharmaceutical products.



[illegible]

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AG	AI	AK	AM	AQ	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
22	00023	00021	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
23	00026	00022	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0					
24	00028	00023	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	90.8	534	1	520	1431	
25	00029	00024	5	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
26	00030	00025	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
27	00031	00026	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
28	00033	00027	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
29	00034	00028	8	1	0	0	0	0	0	0	0	0	0	0	0	1	1	0	1	0	1	1	0	0	0	0						
30	00036	00029	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
31	00037	00030	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
32	00038	00031	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
33	00039	00032	7	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1	0	0	0	0	0	0	2	M7233	95.4	346	1	36	600
34	00040	00033	5	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1						
35	00041	00034	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
36	00042	00035	9	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0						
37	00043	00036	9	2	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
38	00044	00037	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
39	00045	00038	5	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
40	00046	00039	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
41	00047	00040	3	1	0	0	0	0	0	0	0	1	0																			

[illegible]

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AD	AE	AF	AG	AJ	AK	AM	AO	AS	AW	AY	BA	BB	BE	BF	BG	BH	BI	BK
94	00105	00093	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
95	00106	00094	8	2	1	1	0	0	0	0	0	0	0	1	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
96	00107	00095	2	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
97	00108	00096	31	2	3	0	0	1	0	2	0	1	0	3	0	0	0	0	0	0	3	5	2	1	1	0	1	2	0	0	0	0	0	0	
98	00109	00097	5	1	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	
99	00110	00098	2	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
100	00111	00099	38	7	0	0	1	9	13	6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
101	00113	00100	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
102	00114	00101	38	1	1	5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
103	00115	00102	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
104	00116	00103	17	2	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
105	00117	00104	3	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
106	00118	00105	7	4	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
107	00119	00106	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
108	00120	00107	5	2	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
109	00121	00108	4	1	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
110	00122	00109	4	1	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
111	00123	00110	14	2	0	0																													

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AG	AI	AK	AM	AN	AS	AW	AY	BABC	BE	BF	BG	BH	BI	BK
130	00143	00129	5	2	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
131	00144	00130	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
132	00145	00131	2	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
133	00146	00132	8	1	2	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
134	00147	00133	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
135	00148	00134	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
136	00149	00135	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
137	00150	00136	17	2	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
138	00151	00137	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
139	00152	00138	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
140	00153	00139	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
141	00154	00140	5	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
142	00155	00141	81	1	0	3	8	0	3	0	2	3	4	5	1	0	5	15	4	1	2	0	0	0	0	0					
143	00156	00142	20	2	1	0	1	0	0	0	0	0	0	1	1	0	1	0	0	3	0	0	0	0	0	0					
144	00157	00143	11	1	0	0	0	8	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
145	00158	00144	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
146	00159	00145	4	1	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
147	00160	00146	9	1	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1	0	0	1	0	0	0					
148	00161	00147	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
149	00162	00148	47	1	4	3	2	1	0	1	2	5	2	4	4	2	0	2	2	1	7										

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AO	AS	AW	AY	BA	BC	BE	BF	BG	BH	BI	BK
166	00179	00165	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
167	00180	00166	7	2	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
168	00181	00167	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
169	00182	00168	7	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	M34671	99	97	1	1575	1671
170	00183	00169	4	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
171	00184	00170	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
172	00185	00171	13	2	1	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
173	00186	00172	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
174	00187	00173	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
175	00188	00174	11	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
176	00189	00175	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
177	00190	00176	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
178	00191	00177	3	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
179	00192	00178	2	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
180	00193	00179	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
181	00194	00180	34	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
182	00195	00181	4	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
183	00196	00182	67	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
184	00197	00183	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
185	00198	00184	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
186	00199	00185	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
187	00200	00186	4	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
188	00201	00187	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
189	00202	00188	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
190	00203	00189	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
191	00204	00190	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
192	00205	00191	5	2	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
193	00206	00192	7	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
194	00207	00193	5	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
195	00208	00194	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
196	00210	00195	14	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
197	00211	00196	128	8	24	2	10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
198	00212	00197	16	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
199	00213	00198	8	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
200	00215	00199	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
201	00216	00200	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						

Table 6

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AV	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
202	00217	00201	5	1	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
203	00218	00202	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
204	00219	00203	13	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
205	00220	00204	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
206	00221	00205	4	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
207	00222	00206	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
208	00223	00207	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
209	00224	00208	8	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
210	00225	00209	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
211	00226	00210	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
212	00227	00211	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
213	00228	00212	9	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
214	00230	00213	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
215	00231	00214	6	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
216	00232	00215	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
217	00233	00216	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
218	00234	00217	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
219	00235	00218	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
220	00236	00219	11	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
221	00237	00220	11	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
222	00238	00221	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
223	00239	00222	7	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
224	00240	00223	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
225	00241	00224	12	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
226	00242	00225	5	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
227	00243	00226	7	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
228	00244	00227	65	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
229	00245	00228	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
230	00246	00229	26	3	5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
231	00247	00230	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
232	00248	00231	7	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
233	00249	00232	9	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
234	00250	00233	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
235	00251	00234	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
236	00252	00235	5	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
237	00253	00236	16	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Table 7

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AO	AS	AW	AY	BABC	BE	BF	BG	BH	BI	BK
238	00254	00237	38	1	0	0	2	0	0	1	2	1	0	1	0	2	0	1	3	0	0	0	0	1	3	20	0	98.1	214	1	1152	1365
239	00255	00238	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
240	00256	00239	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
241	00257	00240	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
242	00258	00241	6	1	0	0	0	0	1	0	0	0	1	0	0	0	1	0	0	0	1	0	0	1	0	0	95.4	217	3	1857	2077	
243	00259	00242	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
244	00260	00243	4	1	0	0	0	0	0	0	1	0	0	0	1	0	0	0	1	0	0	0	0	0	0	0						
245	00261	00244	17	2	1	0	1	0	0	0	0	0	1	0	1	1	0	0	0	1	0	0	0	0	1	0	99	204	1	1607	1809	
246	00262	00245	50	2	7	2	0	1	1	2	0	3	6	0	1	3	0	3	0	1	2	0	0	4	0	6	98.6	211	1	888	1097	
247	00263	00246	2	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
248	00264	00247	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
249	00265	00248	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
250	00266	00249	3	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1	0	0	0	0	0						
251	00267	00250	6	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	3	99.1	107	83	1	2150	
252	00268	00251	5	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
253	00269	00252	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.3	116	1	1152	1267	
254	00270	00253	9	1	0	1	0	0	0	0	1	0	1	0	3	0	1	0	0	0	0	0	0	0	0	0	95.2	209	1	2887	3088	
255	00271	00254	24	2	0	1	2	0	1	0	0	2	0	0	5	0	1	2	0	1	1	0	0	2	0	4	99	210	1	92	301	
256	00272	00255	9	1	0	0	0	0	0	1	2	0	0	0	1	0	0	0	1	0	1	0	0	0	1	0						







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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AI	AK	AM	AO	AS	AW	AY	B	BC	DE	DF	BG	BH	BI	BK
346	00368	00345	11	1	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1M31627	98.6 141	1	1657	1818		
347	00369	00346	3	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0L10379	98.6 142	1	1581	1725		
348	00370	00347	7	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
349	00372	00348	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
350	00373	00349	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
351	00374	00350	10	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
352	00375	00351	36	2	3	0	0	1	2	0	0	3	5	0	0	0	0	0	0	0	0	0	0	0	6						
353	00376	00352	21	2	0	0	0	1	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	1						
354	00377	00353	2	1	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0						
355	00378	00354	3	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
356	00379	00355	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
357	00380	00356	47	1	12	0	0	1	0	1	3	0	2	0	0	0	0	0	0	0	0	0	0	0	0						
358	00381	00357	22	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
359	00382	00358	4	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
360	00383	00359	28	3	1	3	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
361	00384	00360	10	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
362	00385	00361	4	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
363	00386	00362	6	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
364	00387	00363	5	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
365	00388	00364	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
366	00389	00365	4	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
367	00390	00366	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
368	00391	00367	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
369	00392	00368	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
370	00393	00369	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
371	00394	00370	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
372	00395	00371	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
373	00396	00372	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
374	00397	00373	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
375	00398	00374	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
376	00399	00375	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
377	00400	00376	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
378	00401	00377	16	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
379	00402	00378	39	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
380	00403	00379	21	7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
381	00404	00380	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Table 11

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AE	AG	AI	AK	AM	AO	AS	AT	BA	BC	BE	BF	BG	BH	BI	BK
382	00405	00381	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
383	00406	00382	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
384	00407	00383	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
385	00408	00384	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
386	00409	00385	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
387	00410	00386	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
388	00411	00387	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
389	00412	00388	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
390	00413	00389	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
391	00414	00390	4	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
392	00415	00391	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
393	00416	00392	3	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
394	00417	00393	4	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
395	00418	00394	116	5	22	1	13	1	5	1	0	10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
396	00419	00395	2	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
397	00420	00396	4	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
398	00421	00397	13	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
399	00422	00398	16	1	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
400	00423	00399	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
401	00424	00400	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
402	00425	00401	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
403	00426	00402	13	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
404	00427	00403	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
405	00428	00404	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
406	00429	00405	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
407	00430	00406	3	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
408	00431	00407	4	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
409	00433	00408	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
410	00434	00409	13	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
411	00435	00410	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
412	00436	00411	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
413	00437	00412	34	5	4	2	2	0	0	0	2	1	0	2	1	0	1	2	0	0	0	0	0	0	0	0	0	0	0	0	0
414	00438	00413	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
415	00439	00414	9	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
416	00440	00415	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
417	00441	00416	4	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	

Table 12

Table 13

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AO	AS	AW	BA	BC	BE	BF	BG	BH	BI	BK	
454	00482	00453	7	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100	51	1	2808	2858		
455	00483	00454	5	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
456	00484	00455	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
457	00485	00456	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
458	00486	00457	6	6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
459	00487	00458	11	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
460	00488	00459	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	90	2	61	1	1905	2593	
461	00489	00460	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
462	00491	00461	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
463	00493	00462	4	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
464	00494	00463	4	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
465	00495	00464	12	1	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
466	00496	00465	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
467	00497	00466	11	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
468	00498	00467	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
469	00500	00468	54	6	4	1	1	0	2	2	3	3	2	3	1	1	0	3	8	1	2	1	1	1	1	0	4	94	1	51	1	438	488
470	00503	00469	8	1	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98	1	52	1	1131	1213	
471	00504	00470	56	1	5	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98	1	51	1	1706	1755	
472	00505	00471	7	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	90	50	1	599	647	0	0
473	00506	00472	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
474	00507	00473	9	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
475	00510	00474	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
476	00511	00475	7	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
477	00532	00476	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
478	00533	00477	44	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	92	1	644	1	201	1119	
479	00534	00478	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	93	5	321	1	3091	3727	
480	00535	00479	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
481	00536	00480	4	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
482	00537	00481	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
483	00538	00482	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
484	00539	00483	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
485	00540	00484	4	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
486	00541	00485	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
487	00542	00486	2	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
488	00543	00487	65	9	4	5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	94	8	503	1	4312	4804	
489	00544	00488	5	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98	8	161	1	512	672	

Table 14

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AG	AI	AK	AM	AN	AO	AP	AR	AS	AT	AW	AY	BA	BC	BE	BF	BG	BH	BI	BK	
490	00545	00489	36		3	0	2	0	0	2	1	2	3	0	1	3	1	0	2	1	0	2	1	1	0	1	1	3	0	7	1	94314	93.4	439	1	75	556
491	00546	00490	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
492	00547	00491	3		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
493	00548	00492	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
494	00549	00493	2		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
495	00551	00494	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
496	00552	00495	4		1	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
497	00553	00496	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
498	00554	00497	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
499	00555	00498	4		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
500	00556	00499	2		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
501	00557	00500	2		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
502	00558	00501	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
503	00560	00502	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
504	00561	00503	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
505	00562	00504	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
506	00564	00505	2		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
507	00565	00506	70		4	2	5	0	1	1	1	1	1	4	5	1	1	0	4	6	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	
508	00567	00507	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
509	00568	00508	3		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
510	00569	00509	10		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
511	00571	00510	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
512	00572	00511	2		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
513	00573	00512	2		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
514	00574	00513	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
515	00575	00514	2		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
516	00576	00515	3		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
517	00577	00516	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
518	00578	00517	2		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
519	00579	00518	3		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
520	00580	00519	2		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
521	00581	00520	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
522	00582	00521	2		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
523	00583	00522	34		2	5	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
524	00584	00523	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
525	00585	00524	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	

Table 15

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A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AO	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
526	00586	00525	6	1	0	0	1	1	0	0	0	0	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	2970
527	00589	00526		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2559
528	00590	00527	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1401
529	00591	00528	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1045
530	00592	00529	15	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	174
531	00593	00530	6	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	506
532	00594	00531	17	3	1	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	475
533	00595	00532	4	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1968
534	00596	00533	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2509
535	00597	00534	5	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
536	00598	00535	3	1	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
537	00599	00536	4	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
538	00600	00537	12	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
539	00601	00538	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
540	00602	00539	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
541	00603	00540	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
542	00604	00541	4	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
543	00606	00542	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
544	00607	00543	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
545	00608	00544	22	5	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
546	00609	00545	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
547	00610	00546	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
548	00611	00547	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
549	00612	00548	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
550	00614	00549	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
551	00615	00550	8	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
552	00616	00551	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
553	00617	00552	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
554	00618	00553	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
555	00619	00554	4	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
556	00620	00555	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
557	00621	00556	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
558	00622	00557	3	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
559	00623	00558	4	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
560	00624	00559	3	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
561	00625	00560	4	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	

Table 16



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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AO	AS	AT	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
562	00626	00561	4		2	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
563	00627	00562	2		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
564	00628	00563	4		1	1	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
565	00629	00564	3		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
566	00630	00565	3		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
567	00631	00566	2		2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
568	00632	00567	5		1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
569	00633	00568	3		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
570	00634	00569	2		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
571	00635	00570	2		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
572	00636	00571	5		1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
573	00637	00572	3		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
574	00638	00573	3		1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
575	00639	00574	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
576	00640	00575	10		2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
577	00641	00576	8		2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
578	00642	00577	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
579	00643	00578	2		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
580	00644	00579	24		5	0	2	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
581	00645	00580	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
582	00646	00581	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
583	00647	00582	3		2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
584	00648	00583	8		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
585	00649	00584	3		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
586	00650	00585	52		14	2	6	0	2	0	1	1	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
587	00651	00586	9		4	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
588	00652	00587	2		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
589	00653	00588	13		2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
590	00654	00589	2		2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
591	00655	00590	3		2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
592	00656	00591	3		3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
593	00657	00592	1		1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
594	00658	00593	6		2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
595	00659	00594	9		2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
596	00660	00595	2		2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
597	00661	00596	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						

Table 17

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AI	AK	AM	AO	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
598	00664	00597	3		1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
599	00665	00598	2		1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
600	00666	00599	5		1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.4	248		1	1335	1692	
601	00667	00600	1		1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
602	00668	00601	8		2	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
603	00669	00602	2		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
604	00670	00603	12		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.4	249		1	600	851	
605	00671	00604	3		2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
606	00672	00605	7		3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	97.9	241		1	2915	3319	
607	00673	00606	3		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	96.2	240		1	2728	2969	
608	00674	00607	5		1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
609	00675	00608	31		4	1	4	0	1	0	2	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	100	237		1	291	530	
610	00676	00609	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
611	00677	00610	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
612	00678	00611	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
613	00679	00612	15		1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
614	00680	00613	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
615	00681	00614	7		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100	238		1	2484	2739	
616	00682	00615	3		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.2	254		1	1304	3043	
617	00683	00616	20		1	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	96.1	230		1	194	422	
618	00684	00617	4		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	95.8	237		1	1728	3755	
619	00685	00618	18		2	5	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
620	00686	00619	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
621	00687	00620	16		1	1	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.4	246		1	1494	1741	
622	00688	00621	40		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
623	00689	00622	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
624	00690	00623	3		1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
625	00691	00624	6		2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
626	00692	00625	4		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
627	00693	00626	3		2	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
628	00694	00627	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
629	00695	00628	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
630	00696	00629	7		2	3	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	96.9	226		1	1640	1880	
631	00697	00630	3		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
632	00698	00631	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
633	00699	00632	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
634	00700	00633	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							

Table 18

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AO	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
634	00701	00633	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
635	00702	00634	2		2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
636	00703	00635	17		4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.3	172	1	466	635	
637	00704	00636	45		4	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100	217	1	506	722	
638	00705	00637	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
639	00706	00638	2		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
640	00707	00639	10		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	92.3	209	1	887	1093	
641	00708	00640	32		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
642	00710	00641	2		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.4	127	84	3	135	
643	00711	00642	3		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
644	00712	00643	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
645	00713	00644	3		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
646	00714	00645	13		3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99	202	1	531	732	
647	00715	00646	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
648	00716	00647	48		5	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	94	200	1	291	495	
649	00717	00648	6		1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	97.5	198	1	2231	2444	
650	00718	00649	3		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
651	00719	00650	2		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
652	00720	00651	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
653	00721	00652	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
654	00722	00653	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
655	00723	00654	11		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
656	00725	00655	10		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	97	202	1	509	753	
657	00726	00656	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
658	00727	00657	3		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
659	00728	00658	5		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
660	00729	00659	7		2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	94	204	1	932	1064	
661	00730	00660	4		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
662	00731	00661	2		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
663	00732	00662	47		6	3	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
664	00733	00663	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
665	00734	00664	3		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
666	00735	00665	11		2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
667	00736	00666	2		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
668	00737	00667	3		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
669	00738	00668	6		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						

Table 19

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AO	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
670	00739	00669	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
671	00740	00670	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
672	00741	00671	2	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
673	00742	00672	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
674	00743	00673	54	7	1	7	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
675	00745	00674	4	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
676	00746	00675	13	1	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
677	00747	00676	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
678	00748	00677	5	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
679	00749	00678	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
680	00750	00679	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
681	00751	00680	5	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
682	00752	00681	4	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
683	00753	00682	6	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
684	00754	00683	5	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
685	00755	00684	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
686	00757	00685	5	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
687	00758	00686	5	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
688	00759	00687	25	4	1	1	0	0	1	1	0	0	2	1	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
689	00760	00688	10	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
690	00761	00689	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
691	00762	00690	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
692	00763	00691	3	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
693	00764	00692	6	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
694	00765	00693	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
695	00766	00694	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
696	00768	00695	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
697	00769	00696	8	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
698	00770	00697	4	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
699	00771	00698	3	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
700	00772	00699	6	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
701	00773	00700	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
702	00774	00701	5	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
703	00775	00702	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
704	00777	00703	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
705	00778	00704	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	

Table 20

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AO	AS	AW	AY	BABC	BE	BF	BGBH	BI	BK	
706	00779	00705	3	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0X5568	92.6	149	1	824	965	
707	00780	00706	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0X70944	100	152	1	2916	3071	
708	00781	00707	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
709	00782	00708	8	1	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	
710	00783	00709	5	1	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	
711	00784	00710	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
712	00785	00711	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0M37716	100	145	1	329	491	
713	00786	00712	4	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
714	00787	00713	8	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
715	00788	00714	4	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
716	00789	00715	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0M15502	96.5	141	1	1310	1447	
717	00790	00716	5	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0X59417	96.6	149	1	824	979	
718	00791	00717	6	1	0	0	0	0	0	0	0	0	1	1	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
719	00792	00718	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
720	00793	00719	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
721	00794	00720	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
722	00795	00721	42	1	1	2	0	1	3	0	5	0	2	0	4	5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
723	00796	00722	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
724	00797	00723	36	4	0	1	0	2	1	0	1																					





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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK	
814	00891	00813	5	1	0	0	0	0	0	0	0	1	0	0	1	0	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	
815	00892	00814	4	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
816	00894	00815	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
817	00895	00816	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
818	00896	00817	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
819	00897	00818	10	2	1	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
820	00898	00819	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
821	00900	00820	27	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
822	00903	00821	3	1	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
823	00904	00822	8	1	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
824	00905	00823	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
825	00906	00824	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
826	00908	00825	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
827	00910	00826	2	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
828	00911	00827	9	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
829	00912	00828	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
830	00913	00829	5	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
831	00914	00830	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
832	00915	00831	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
833	00917	00832	43	3	1	0	0	0	0	0	0	2	1	1	5	6	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
834	00918	00833	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
835	00919	00834	7	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
836	00920	00835	4	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
837	00922	00836	9	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
838	00924	00837	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
839	00925	00838	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
840	00926	00839	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
841	00929	00840	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
842	00930	00841	4	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
843	00931	00842	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
844	00932	00843	16	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
845	00934	00844	34	3	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
846	00935	00845	6	1	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
847	00936	00846	8	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
848	00937	00847	62	1	5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
849	00938	00848	8	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	

Table 24



	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AN	AO	AS	AW	AY	BABC	BE	BF	BG	BH	BI	BK
850	00955	00849	6		3	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
851	00972	00850	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
852	00973	00851	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
853	00974	00852	59		0	2	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	5	1	6	2	0						
854	00976	00853	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
855	00977	00854	5		0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
856	00978	00855	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
857	00979	00856	3		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
858	00980	00857	12		0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
859	00981	00858	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
860	00982	00859	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
861	00983	00860	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
862	00984	00861	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
863	00985	00862	2		0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
864	00986	00863	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
865	00987	00864	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
866	00988	00865	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
867	00989	00866	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
868	00990	00867	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
869	00991	00868	1		0	1	0	0																									



	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AG	AI	AK	AM	AQ	AS	AW	AY	B	BC	DE	DF	BGBH	BI	BK	
922	01048	00921	5		0	1	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	1	0	0	96.9	382	1	708	1089
923	01049	00922	2	0	0	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
924	01051	00923	3	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1	0						
925	01052	00924	3	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
926	01053	00925	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	90.3	380	24	3711	4221	
927	01054	00926	2	0	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
928	01055	00927	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
929	01057	00928	3	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
930	01061	00929	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.3	347	1	1115	1460	
931	01062	00930	8	0	1	1	0	0	0	0	0	0	1	0	0	1	0	0	0	0	2	1	0	1	0	0	97.2	394	1	1011	1441	
932	01063	00931	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
933	01064	00932	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
934	01065	00933	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
935	01066	00934	2	0	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
936	01067	00935	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
937	01068	00936	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
938	01069	00937	2	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
939	01070	00938	2	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
940	01071	00939	2	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
941	01072	00940	8	0	2	0	0	0																								



Table 29









[illegible]

[illegible]

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AO	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
1210	01355	01209	2		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1211	01356	01210	2		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1212	01357	01211	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1213	01358	01212	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	95.3	127	1	453	579	
1214	01359	01213	2		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1215	01360	01214	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1216	01361	01215	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1217	01362	01216	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1218	01363	01217	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1219	01364	01218	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1220	01365	01219	4		0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1221	01366	01220	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1222	01367	01221	21		0	0	3	1	0	0	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1223	01368	01222	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1224	01369	01223	5		0	0	1	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1225	01370	01224	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1226	01371	01225	5		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1227	01372	01226	7		0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1228	01373	01227	2		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1229	01374	01228	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1230	01375	01229	2		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1231	01377	01230	3		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1232	01378	01231	5		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1233	01379	01232	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1234	01380	01233	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1235	01381	01234	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1236	01382	01235	5		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1237	01383	01236	3		0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1238	01384	01237	16		0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1239	01385	01238	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1240	01386	01239	3		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1241	01387	01240	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1242	01388	01241	3		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1243	01389	01242	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1244	01390	01243	5		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1245	01391	01244	2		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						

Table 35

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AW	AY	BABC	BE	BF	BG	BH	BI	BK
1246	01392	01245	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0X03342	90.7	161	1	67	505	
1247	01393	01246	5		0	1	0	0	0	1	0	0	0	0	0	1	0	0	0	0	0	0	1	0	0	0						
1248	01394	01247	12		0	4	0	0	0	0	1	2	0	0	1	1	0	0	0	0	0	0	0	0	0	0						
1249	01395	01248	7		0	1	1	2	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0Z17227	100	152	1	1724	1875	
1250	01396	01249	4		0	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0						
1251	01397	01250	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1252	01398	01251	2		0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1253	01400	01252	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1254	01401	01253	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1255	01402	01254	7		0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1256	01403	01255	6		0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1257	01404	01256	16		0	2	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0						
1258	01405	01257	4		0	1	0	0	0	0	0	2	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0M93651	96.2	159	1	1551	2577
1259	01406	01258	7		0	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1260	01407	01259	3		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1261	01408	01260	3		0	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
1262	01409	01261	5		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1263	01410	01262	2		0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1264	01411	01263	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1265	01412	01264	1		0	1	0	0	0	0																						





[illegible]





	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
1426	01579	01425	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1427	01580	01426	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1428	01581	01427	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1429	01582	01428	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1430	01583	01429	5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1431	01584	01430	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1432	01585	01431	8	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1433	01586	01432	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1434	01587	01433	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1435	01588	01434	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1436	01589	01435	10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1437	01590	01436	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1438	01591	01437	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1439	01592	01438	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1440	01593	01439	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1441	01594	01440	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1442	01595	01441	7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1443	01596	01442	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1444	01597	01443	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1445	01598	01444	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1446	01599	01445	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1447	01600	01446	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1448	01601	01447	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1449	01602	01448	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1450	01603	01449	5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1451	01604	01450	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1452	01605	01451	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1453	01606	01452	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1454	01607	01453	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1455	01608	01454	23	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1456	01609	01455	16	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1457	01610	01456	5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1458	01611	01457	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1459	01612	01458	5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1460	01614	01459	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1461	01615	01460	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	

Table 41





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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AO	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
1534	01746	01533	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1535	01747	01534	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1536	01748	01535	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1537	01749	01536	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1538	01750	01537	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1539	01751	01538	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1540	01752	01539	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1541	01753	01540	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1542	01754	01541	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1543	01755	01542	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1544	01756	01543	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1545	01758	01544	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1546	01759	01545	7		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1547	01760	01546	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1548	01761	01547	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1549	01763	01548	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1550	01764	01549	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1551	01765	01550	7		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1552	01766	01551	63		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1553	01767	01552	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1554	01768	01553	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1555	01769	01554	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1556	01770	01555	5		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1557	01771	01556	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1558	01772	01557	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1559	01773	01558	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1560	01774	01559	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1561	01775	01560	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1562	01776	01561	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1563	01777	01562	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1564	01778	01563	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1565	01779	01564	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1566	01780	01565	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1567	01781	01566	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1568	01782	01567	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1569	01783	01568	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							

Table 44

[illegible]



[illegible]





	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AI	AJ	AK	AM	AO	AS	AT	AW	AY	BA	BB	BC	BE	BF	BG	BH	BI	BK
1714	01930	01713	2	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
1715	01931	01714	4	0	0	0	0	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1716	01932	01715	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1717	01933	01716	10	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1718	01934	01717	5	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1719	01935	01718	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1720	01936	01719	2	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1721	01937	01720	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1722	01938	01721	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1723	01939	01722	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1724	01940	01723	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1725	01941	01724	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1726	01943	01725	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1727	01944	01726	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1728	01945	01727	7	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1729	01946	01728	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1730	01947	01729	6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1731	01948	01730	4	0	0	0	0	0	1	0	0	0</																								



Table 51



[illegible]





[illegible]





[illegible]

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AW	AY	BA	BC	BE	BF	BG	BI	BK
2074	02358	02073	2		0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	X69078	97.9	95	1	3127	3228
2075	02359	02074	2		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
2076	02360	02075	3		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0						
2077	02361	02076	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2078	02362	02077	4		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2079	02363	02078	2		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2080	02364	02079	1		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2081	02365	02080	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2082	02366	02081	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2083	02367	02082	2		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2084	02368	02083	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2085	02369	02084	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2086	02370	02085	2		0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2087	02371	02086	1		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2088	02372	02087	6		0	0	0	0	1	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0						
2089	02373	02088	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2090	02374	02089	38		0	0	0	0	1	1	1	5	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
2091	02375	02090	1		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2092	02376	02091	4		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2093	02377	02092	1		0	0	0																									

[illegible]





Table 63





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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AW	AY	BA	BC	BE	BF	BG	BH	BI	BK
2290	02645	02289	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2291	02646	02290	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2292	02648	02291	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2293	02650	02292	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2294	02651	02293	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2295	02652	02294	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	97.3	331	1	1560	1902
2296	02653	02295	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2297	02654	02296	2		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2298	02656	02297	20		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2299	02657	02298	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	92.3	351	1	962	1304
2300	02658	02299	6		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2301	02659	02300	2		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2302	02660	02301	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2303	02661	02302	3		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2304	02662	02303	2		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2305	02663	02304	4		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2306	02664	02305	5		0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	91.5	319	1	1004	1778
2307	02665	02306	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	97.9	233	1	4204	5200
2308	02666	02307	2		0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2309	02667	02308	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2310	02668	02309	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2311	02669	02310	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2312	02670	02311	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2313	02672	02312	5		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2314	02673	02313	5		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.8	320	2	1957	2277
2315	02675	02314	2		0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2316	02676	02315	2		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2317	02677	02316	2		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2318	02678	02317	2		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2319	02679	02318	2		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2320	02680	02319	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99	303	1	541	849
2321	02681	02320	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2322	02682	02321	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	97	296	1	2232	2527
2323	02684	02322	13		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	96.1	284	1	5182	5722
2324	02685	02323	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2325	02686	02324	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					

Table 65





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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AG	AK	AM	AN	AS	AW	AY	BA	BC	BE	BF	BG	BI	BK
2398	02765	02397	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
2399	02767	02398	9		0	0	0	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0				
2400	02768	02399	5		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
2401	02769	02400	7		0	0	0	0	0	0	1	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
2402	02770	02401	3		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
2403	02771	02402	2		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
2404	02772	02403	2		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
2405	02773	02404	2		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
2406	02774	02405	3		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
2407	02775	02406	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
2408	02776	02407	2		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
2409	02777	02408	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			2493	
2410	02778	02409	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			1 2077	
2411	02779	02410	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
2412	02780	02411	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
2413	02781	02412	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
2414	02782	02413	3		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
2415	02783	02414	5		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
2416	02785	02415	2		0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			1391	
2417	02786	02416	2		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			1 1230	
2418	02787	02417	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
2419	02788	02418	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
2420	02789	02419	3		0	0	0	0	0	0	1	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
2421	02790	02420	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			1 1219	
2422	02791	02421	3		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			1 3744	
2423	02792	02422	4		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			99 192	
2424	02793	02423	9		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			97 9 192	
2425	02794	02424	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
2426	02795	02425	7		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
2427	02796	02426	5		0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
2428	02797	02427	3		0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
2429	02798	02428	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
2430	02799	02429	3		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
2431	02800	02430	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
2432	02801	02431	9		0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
2433	02802	02432	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			98 2 171	
																													1 1230	
																													1410	

Table 68

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AW	AY	BA	BC	BE	BF	BG	BI	BK			
2434	02803	02433	2		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0							
2435	02804	02434	5		0	0	0	0	0	0	0	2	1	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0							
2436	02805	02435	4		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0							
2437	02806	02436	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
2438	02807	02437	2		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
2439	02808	02438	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	X70991	95.4	174	1	2015	2192	
2440	02809	02439	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
2441	02810	02440	2		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
2442	02811	02441	4		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
2443	02812	02442	12		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	D14665	100	165	1	3377	3541	
2444	02813	02443	5		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2445	02814	02444	15		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2446	02815	02445	4		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2447	02816	02446	2		0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2448	02817	02447	2		0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2449	02818	02448	5		0	0	0	0	0	0	0	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2450	02819	02449	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2451	02820	02450	29		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	X02490	91.9	135	14	435	568
2452	02821																																		

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AI	AK	AM	AO	AS	AW	AY	BA	BC	BE	BF	BG	BI	BI	BK
2470	02839	02469	2		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
2471	02840	02470	3		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2472	02843	02471	2		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2473	02844	02472	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2474	02845	02473	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2475	02846	02474	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2476	02847	02475	11		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2477	02848	02476	2		0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2478	02849	02477	2		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2479	02850	02478	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2480	02851	02479	9		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2481	02852	02480	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2482	02853	02481	8		0	0	0	0	0	0	2	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2483	02854	02482	4		0	0	0	0	0	0	2	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2484	02855	02483	2		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2485	02856	02484	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2486	02857	02485	3		0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2487	02858	02486	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2488	02859	02487	5		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2489	02860	02488	4		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2490	02861	02489	10		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2491	02862	02490	7		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2492	02863	02491	3		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2493	02864	02492	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2494	02865	02493	2		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2495	02866	02494	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2496	02867	02495	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2497	02868	02496	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2498	02869	02497	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2499	02870	02498	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2500	02872	02499	4		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2501	02873	02500	5		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2502	02874	02501	6		0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2503	02875	02502	2		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2504	02876	02503	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2505	02877	02504	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					

Table 70







[illegible]





[illegible]





[illegible]





	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AI	AG	AK	AM	AQ	AS	AV	AY	BA	BC	BE	BF	BG	BH	BI	BK
2866	03406	02865	2	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0						
2867	03407	02866	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
2868	03408	02867	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
2869	03409	02868	2	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0						
2870	03410	02869	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
2871	03411	02870	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
2872	03412	02871	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
2873	03413	02872	3	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0						
2874	03414	02873	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
2875	03415	02874	2	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0						
2876	03416	02875	4	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
2877	03417	02876	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
2878	03418	02877	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
2879	03419	02878	7	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
2880	03420	02879	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
2881	03421	02880	4	0	0	0	0	0	0	0	0	0	2	1	0	0	0	0	0	0	0	0	0	0	0	0						
2882	03422	02881	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
2883	03423	02882	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
2884	03424	02883	4	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
2885	03425	02884	1	0	0																											

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AI	AK	AM	AN	AO	AS	AT	AV	AW	AY	BABC	BE	BF	BG	BH	BI	BK		
2902	03443	02901	14		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	3	4	1	0	0	0	0	5	0	0	0						
2903	03444	02902	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2904	03445	02903	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2905	03446	02904	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2906	03447	02905	5	0	0	0	0	0	0	0	0	0	1	0	1	1	0	0	0	0	0	0	0	1	0	0	1	0	0	0	554769	96.2	264	1	161	429	
2907	03448	02906	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2908	03449	02907	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2909	03450	02908	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2910	03451	02909	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2911	03452	02910	2	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
2912	03453	02911	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2913	03454	02912	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2914	03455	02913	5	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1	0	3	0	0	0	0	0	0	0	0						
2915	03456	02914	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2916	03457	02915	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2917	03458	02916	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2918	03459	02917	7	0	0	0	0	0	0	0	0	0	2	4	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	95.1	247	1	1311	1557

[illegible]

	A	B.	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AJ	AK	AM	AO	AS	AT	AV	AW	AY	BABC	BE	BF	BG	BH	BI	BK
2974	03516	02973	3		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	1	0	0	1	0	0	0	0	0	0					
2975	03517	02974	10		0	0	0	0	0	0	0	0	4	0	0	0	0	0	1	0	0	0	0	1	0	0	0	0	0					
2976	03518	02975	2		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	100	96	1	1335	
2977	03519	02976	2		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0					
2978	03520	02977	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2979	03521	02978	3		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	97.6	166	1	2428	
2980	03522	02979	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
2981	03523	02980	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2982	03524	02981	3		0	0	0	0	0	0	0	0	1	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0					
2983	03525	02982	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2984	03526	02983	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2985	03527	02984	4		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0					
2986	03528	02985	4		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0					
2987	03529	02986	6		0	0	0	0	0	0	0	0	1	0	0	0	1	0	0	2	0	1	1	0	0	0	0	0	0					
2988	03530	02987	2		0	0	0	0	0	0	0	0	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
2989	03531	02988	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2990	03532	02989	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2991	03533	02990	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2992	03534	02991	2		0	0	0	0</																										



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3118	03683	03117	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	97.3	300	1	388	853	
3119	03684	03118	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
3120	03685	03119	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
3121	03686	03120	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
3122	03688	03121	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
3123	03689	03122	5		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
3124	03690	03123	4		0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	104	164				
3125	03691	03124	3		0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0					
3126	03693	03125	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3127	03694	03126	10		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3128	03695	03127	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3129	03696	03128	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3130	03697	03129	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3131	03698	03130	13		0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0					
3132	03699	03131	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3133	03701	03132	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3134	03702	03133	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3135	03703	03134	2		0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0					
3136	03704	03135	3		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3137	03705	03136	3		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3138	03707	03137	3		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3139	03708	03138	4		0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0					
3140	03709	03139	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3141	03710	03140	4		0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0					
3142	03711	03141	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3143	03712	03142	3		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3144	03713	03143	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3145	03714	03144	2		0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0					
3146	03715	03145	3		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3147	03716	03146	4		0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0					
3148	03717	03147	5		0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0					
3149	03718	03148	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3150	03719	03149	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3151	03720	03150	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3152	03721	03151	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3153	03722	03152	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					

Table 88





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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AI	AK	AM	AO	AS	AW	AY	BA	BC	BE	BF	BG	BH	BI	BK
3190	03760	03189	1											1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3191	03761	03190	4											0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3192	03762	03191	2											2	0	0	0	0	0	0	0	0	0	0	0	0	0						
3193	03763	03192	2											1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3194	03764	03193	1											1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3195	03765	03194	1											1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3196	03766	03195	1											1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3197	03767	03196	1											1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3198	03768	03197	3											1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3199	03769	03198	1											1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3200	03770	03199	1											1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3201	03771	03200	1											1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3202	03772	03201	1											1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3203	03773	03202	1											1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3204	03774	03203	2											1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3205	03775	03204	5											1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3206	03776	03205	1											1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3207	03777	03206	2											1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3208	03778	03207	1											1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3209	03779	03208	1											1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3210	03780	03209	3											1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3211	03781	03210	4											1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3212	03782	03211	3											1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3213	03783	03212	1											1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3214	03784	03213	3											1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3215	03785	03214	1											1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3216	03786	03215	2											2	0	0	0	0	0	0	0	0	0	0	0	0	0						
3217	03787	03216	4											1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3218	03788	03217	3											1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3219	03789	03218	6											1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3220	03790	03219	2											1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3221	03791	03220	1											1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3222	03792	03221	1											1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3223	03793	03222	1											2	0	0	0	0	0	0	0	0	0	0	0	0	0						
3224	03794	03223	5											2	0	0	0	0	0	0	0	0	0	0	0	0	0						
3225	03795	03224	2											1	0	0	0	0	0	0	0	0	0	0	0	0	0						

Table 90

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AI	AK	AM	AO	AS	AV	AW	AY	BA	BC	BE	BF	BG	BH	BI	BK
3226	03796	03225	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3227	03797	03226	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3228	03798	03227	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3229	03799	03228	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3230	03800	03229	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3231	03801	03230	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3232	03802	03231	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3233	03803	03232	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3234	03804	03233	7		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3235	03805	03234	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3236	03806	03235	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3237	03807	03236	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3238	03808	03237	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3239	03809	03238	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3240	03810	03239	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3241	03811	03240	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3242	03812	03241	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3243	03813	03242	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3244	03814	03243	6		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3245	03815	03244	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3246	03816	03245	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3247	03817	03246	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3248	03818	03247	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3249	03819	03248	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3250	03820	03249	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3251	03821	03250	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3252	03822	03251	5		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3253	03823	03252	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3254	03824	03253	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3255	03825	03254	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3256	03826	03255	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3257	03827	03256	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3258	03828	03257	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3259	03829	03258	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3260	03830	03259	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3261	03831	03260	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	

Table 91

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AO	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
3262	03832	03261	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3263	03833	03262	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3264	03835	03263	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3265	03836	03264	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3266	03837	03265	13		0	0	0	0	0	0	0	0	0	5	0	0	0	0	0	0	0	0	0	0	0	0	0						
3267	03838	03266	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3268	03839	03267	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3269	03840	03268	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3270	03841	03269	3		0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0						
3271	03842	03270	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3272	03843	03271	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3273	03844	03272	50		0	0	0	0	0	0	0	0	0	25	0	0	0	0	0	0	0	0	0	0	0	0	0						
3274	03845	03273	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3275	03846	03274	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3276	03847	03275	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3277	03848	03276	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3278	03849	03277	3		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3279	03850	03278	2		0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0						
3280	03851	03279	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3281	03852	03280	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3282	03853	03281	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3283	03854	03282	2		0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0						
3284	03855	03283	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3285	03856	03284	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3286	03857	03285	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3287	03859	03286	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3288	03860	03287	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3289	03861	03288	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3290	03862	03289	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3291	03863	03290	3		0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0						
3292	03864	03291	6		0	0	0	0	0	0	0	0	0	1	1	2	0	0	0	0	0	0	0	0	0	0	0						
3293	03865	03292	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3294	03866	03293	3		0	0	0	0	0	0	0	0	0	2	1	0	0	0	0	0	0	0	0	0	0	0	0						
3295	03867	03294	20		0	0	0	0	0	0	0	0	0	2	1	0	0	0	0	0	0	0	0	0	0	0	0						
3296	03868	03295	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3297	03869	03296	7		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						

Table 92

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AD	AG	AI	AK	AM	AN	AO	AS	AT	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
3298	03870	03297	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3299	03871	03298	3	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3300	03872	03299	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3301	03873	03300	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3302	03874	03301	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3303	03875	03302	2	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3304	03876	03303	5	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3305	03877	03304	2	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3306	03878	03305	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3307	03879	03306	7	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3308	03880	03307	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3309	03881	03308	2	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3310	03882	03309	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3311	03883	03310	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3312	03884	03311	2	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3313	03885	03312	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3314	03886	03313	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3315	03887	03314	2	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3316	03888	03315	5	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3317	03889	03316	4	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3318	03890	03317	3	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3319	03891	03318	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3320	03892	03319	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3321	03893	03320	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3322	03894	03321	5	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3323	03895	03322	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3324	03896	03323	7	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3325	03897	03324	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3326	03898	03325	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3327	03899	03326	4	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3328	03900	03327	2	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3329	03901	03328	5	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3330	03902	03329	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3331	03903	03330	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3332	03904	03331	5	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3333	03905	03332	5	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	

Table 93

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AN	AO	AP	AQ	AS	AT	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
3334	03906	03333	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3335	03907	03334	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3336	03908	03335	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3337	03909	03336	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3338	03910	03337	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3339	03911	03338	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3340	03912	03339	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3341	03913	03340	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3342	03914	03341	4		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3343	03915	03342	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3344	03916	03343	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3345	03917	03344	5		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3346	03918	03345	3		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3347	03919	03346	3		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3348	03920	03347	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3349	03921	03348	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3350	03922	03349	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3351	03923	03350	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3352	03924	03351	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3353	03925	03352	4		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3354	03926	03353	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3355	03927	03354	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3356	03928	03355	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3357	03929	03356	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3358	03930	03357	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3359	03931	03358	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3360	03932	03359	5		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3361	03933	03360	3		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3362	03934	03361	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3363	03935	03362	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3364	03936	03363	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3365	03937	03364	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3366	03938	03365	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3367	03939	03366	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3368	03940	03367	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3369	03941	03368	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	

Table 94

Table 95







[illegible]

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AJ	AK	AM	AO	AS	AW	AY	BA	BB	BE	BF	BG	BI	BK
3514	04125	03513	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3515	04126	03514	2		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3516	04127	03515	4		0	0	0	0	0	0	0	0	0	0	1	0	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
3517	04128	03516	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3518	04129	03517	4		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3519	04130	03518	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3520	04131	03519	2		0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3521	04132	03520	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3522	04133	03521	7		0	0	0	0	0	0	0	0	0	0	1	0	1	0	0	0	2	0	1	0	0	1	0	0	0	0	0	0
3523	04134	03522	3		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
3524	04135	03523	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3525	04136	03524	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3526	04137	03525	2		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3527	04139	03526	2		0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3528	04140	03527	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3529	04141	03528	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3530	04142	03529	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3531	04143	03530	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3532	04144	03531	11		0	0	0	0	0																							





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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AO	AS	AW	AY	BA	BC	BE	BF	BG	BH	BI	BK
3622	04273	03621	1													1																	
3623	04274	03622	1													1																	
3624	04275	03623	2													1																	
3625	04276	03624	1													1																	
3626	04278	03625	4													2																	
3627	04279	03626	1													1																	
3628	04280	03627	1													1																	
3629	04281	03628	1													1																	
3630	04282	03629	1													1																	
3631	04284	03630	1													1																	
3632	04285	03631	1													1																	
3633	04286	03632	1													1																	
3634	04287	03633	2													1																	
3635	04288	03634	3													1																	
3636	04289	03635	2													1																	
3637	04290	03636	8													1																	
3638	04291	03637	1													1																	
3639	04292	03638	1													1																	
3640	04293	03639	2													1																	
3641	04294	03640	6													2																	
3642	04295	03641	2													2																	
3643	04296	03642	2													2																	
3644	04297	03643	1													1																	
3645	04298	03644	1													1																	
3646	04299	03645	1													1																	
3647	04300	03646	1													1																	
3648	04302	03647	2													1																	
3649	04303	03648	1													1																	
3650	04304	03649	1													1																	
3651	04305	03650	3													1																	
3652	04306	03651	1													1																	
3653	04307	03652	2													1																	
3654	04308	03653	1													1																	
3655	04309	03654	2													1																	
3656	04310	03655	1													1																	
3657	04311	03656	3													2																	

Table 102



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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AI	AK	AM	AO	AS	AW	AY	B	BC	BE	BF	BG	BI	BK
3694	04349	03693	1																											
3695	04351	03694	1																											
3696	04352	03695	1																											
3697	04353	03696	1																											
3698	04354	03697	4																											
3699	04355	03698	1																											
3700	04356	03699	1																											
3701	04357	03700	2																											
3702	04358	03701	1																											
3703	04359	03702	1																											
3704	04360	03703	2																											
3705	04361	03704	1																											
3706	04362	03705	2																											
3707	04363	03706	2																											
3708	04364	03707	2																											
3709	04365	03708	1																											
3710	04366	03709	1																											
3711	04368	03710	1																											
3712	04369	03711	1																											
3713	04370	03712	2																											
3714	04371	03713	1																											
3715	04372	03714	3																											
3716	04373	03715	3																											
3717	04374	03716	2																											
3718	04375	03717	2																											
3719	04377	03718	2																											
3720	04378	03719	1																											
3721	04379	03720	1																											
3722	04380	03721	1																											
3723	04381	03722	1																											
3724	04382	03723	1																											
3725	04383	03724	1																											
3726	04384	03725	1																											
3727	04385	03726	1																											
3728	04386	03727	3																											
3729	04387	03728	2																											

Table 104



	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AI	AG	AK	AM	AQ	AS	AW	AY	BA	BC	BE	BF	BG	BI	BK
3730	04388	03729	1																												
3731	04389	03730	3																												
3732	04390	03731	2																												
3733	04391	03732	3																												
3734	04392	03733	1																												
3735	04393	03734	3																												
3736	04394	03735	1																												
3737	04395	03736	2																												
3738	04396	03737	1																												
3739	04397	03738	1																												
3740	04398	03739	1																												
3741	04399	03740	1																												
3742	04400	03741	1																												
3743	04401	03742	1																												
3744	04402	03743	7																												
3745	04403	03744	1																												
3746	04404	03745	1																												
3747	04405	03746	2																												
3748	04406	03747	1																												
3749	04407	03748	3																												
3750	04408	03749	1																												
3751	04409	03750	1																												
3752	04410	03751	1																												
3753	04411	03752	2																												
3754	04412	03753	2																												
3755	04414	03754	5																												
3756	04415	03755	3																												
3757	04416	03756	1																												
3758	04417	03757	2																												
3759	04418	03758	2																												
3760	04419	03759	1																												
3761	04420	03760	1																												
3762	04421	03761	2																												
3763	04422	03762	1																												
3764	04423	03763	1																												
3765	04424	03764	1																												

Table 105











[illegible]

[illegible]



[illegible]

[illegible]

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AI	AK	AM	AQ	AS	AW	AY	BZ	BC	BE	BF	BG	BH	BI	BJ
4090	04819	04089	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4091	04820	04090	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4092	04821	04091	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4093	04822	04092	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4094	04823	04093	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4095	04824	04094	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4096	04826	04095	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4097	04827	04096	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4098	04828	04097	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4099	04829	04098	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4100	04830	04099	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4101	04831	04100	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4102	04832	04101	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4103	04833	04102	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4104	04834	04103	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4105	04835	04104	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4106	04836	04105	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4107	04837	04106	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4108	04838	04107	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4109	04839	04108	1		0																												













	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	CA	TA	GA	IA	KA	MA	QA	SA	TA	VA	WA	X	Y	BZ	BI	BK
4306	05119	04305	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0			
4307	05120	04306	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0			
4308	05121	04307	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0			
4309	05122	04308	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
4310	05123	04309	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0			
4311	05124	04310	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0			
4312	05127	04311	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0			
4313	05128	04312	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0			
4314	05129	04313	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0			
4315	05130	04314	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0			
4316	05132	04315	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0			
4317	05133	04316	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0			
4318	05134	04317	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0			
4319	05135	04318	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0			
4320	05136	04319	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0			
4321	05137	04320	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0			
4322	05138	04321	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0			
4323	05139	04322	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0			
4324	05140	04323	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0			
4325	05141	04324	1	0	0	0	0</																								



[illegible]

Table 123





[illegible]

[illegible]

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AI	AK	AM	AO	AS	AW	AY	B	BC	RE	BF	BG	BH	BI	BK
4558	05409	04557	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0							
4559	05410	04558	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0							
4560	05411	04559	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1	1	0	0	0						
4561	05412	04560	9	0	0	0	0	0	0	0	0	0	0	0	0	0	0	7	0	0	0	0	0	0	0	0	0						
4562	05413	04561	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	2	0	0	0	0	0	0						
4563	05414	04562	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0						
4564	05415	04563	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0						
4565	05416	04564	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	2	0	0	0	0						
4566	05417	04565	5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0						
4567	05418	04566	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0						
4568	05419	04567	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0						
4569	05420	04568	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0						
4570	05421	04569	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0						
4571	05422	04570	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
4572	05423	04571	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0	0						
4573	05424	04572	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0						
4574	05425	04573	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0						
4575	05427	04574	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0						
4576	05428	04575	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0						
4577																																	









[illegible]

[illegible]









	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AI	AG	AJ	AK	AM	AN	AS	AW	BA	BC	BE	BF	BG	BH	BI	BK
4882	05816	04881	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4883	05817	04882	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4884	05818	04883	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4885	05819	04884	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4886	05820	04885	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4887	05821	04886	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4888	05823	04887	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4889	05824	04888	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4890	05825	04889	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	X15183	97.8	321	1	2133	2912
4891	05826	04890	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4892	05827	04891	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4893	05829	04892	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4894	05830	04893	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4895	05831	04894	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4896	05832	04895	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4897	05833	04896	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4898	05834	04897	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4899	05835	04898	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4900	05836	04899	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4901	05837	04900	2		0	0	0																									



[illegible]

Table 139

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AI	AK	AM	AN	AO	AS	AT	AW	AY	BABC	BE	BF	BG	BH	BI	BK
4990	05953	04989	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4991	05954	04990	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4992	05955	04991	5		0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4993	05956	04992	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4994	05957	04993	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4995	05959	04994	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4996	05960	04995	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4997	05961	04996	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4998	05962	04997	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4999	05963	04998	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5000	05964	04999	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5001	05966	05000	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5002	05967	05001	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5003	05968	05002	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5004	05969	05003	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5005	05970	05004	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5006	05974	05005	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5007	05975	05006	1		0	0	0	0	0																									

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AG	AI	AK	AM	AQ	AS	AW	AY	BABC	DE	BF	BGBH	BI	BK
5170	06173	05169	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5171	06174	05170	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5172	06175	05171	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5173	06176	05172	3		0	0	0	0	0	0	0	0	0	2	0	0	0	0	1	0	0	0	0	0	0					
5174	06177	05173	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5175	06179	05174	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5176	06180	05175	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5177	06181	05176	2		0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0					
5178	06182	05177	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5179	06183	05178	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5180	06184	05179	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5181	06185	05180	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5182	06186	05181	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	2					
5183	06187	05182	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5184	06188	05183	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5185	06189	05184	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5186	06190	05185	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5187	06191	05186	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5188	06192	05187	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5189	06195	05188	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5190	06196	05189	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5191	06197	05190	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0					
5192	06198	05191	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5193	06199	05192	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5194	06200	05193	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5195	06201	05194	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5196	06202	05195	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5197	06203	05196	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5198	06204	05197	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5199	06205	05198	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5200	06206	05199	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5201	06207	05200	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5202	06208	05201	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5203	06209	05202	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0					
5204	06210	05203	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5205	06211	05204	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AJ	AK	AM	AQ	AS	AW	AY	BA	BC	BE	BF	BG	BH	BI	BK
5206	06213	05205	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0					
5207	06215	05206	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0					
5208	06216	05207	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0					
5209	06217	05208	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0					
5210	06218	05209	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0					
5211	06219	05210	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0					
5212	06220	05211	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1	0	0	0	0	0					
5213	06221	05212	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0					
5214	06222	05213	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0					
5215	06224	05214	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0					
5216	06225	05215	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0					
5217	06226	05216	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0					
5218	06227	05217	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0					
5219	06228	05218	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0					
5220	06229	05219	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0					
5221	06230	05220	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0					
5222	06232	05221	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0					
5223	06233	05222	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0					
5224	06234	05223	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0					
5225	06235	05224	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0					
5226	06236	05225	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0					
5227	06237	05226	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0					
5228	06238	05227	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0					
5229	06240	05228	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0					
5230	06241	05229	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0					
5231	06243	05230	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0					
5232	06244	05231	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0					
5233	06246	05232	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0					
5234	06247	05233	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0					
5235	06248	05234	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0					
5236	06249	05235	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0					
5237	06250	05236	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0					
5238	06251	05237	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0					
5239	06253	05238	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0					
5240	06254	05239	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0					
5241	06255	05240	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0					



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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AF	AG	AI	AK	AM	AQ	AS	AW	AY	BA	BC	BE	BF	BG	BH	BI	BK
5278	06299	05277	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5279	06300	05278	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5280	06301	05279	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5281	06302	05280	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5282	06303	05281	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5283	06304	05282	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5284	06305	05283	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5285	06306	05284	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5286	06307	05285	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5287	06308	05286	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5288	06309	05287	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5289	06310	05288	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5290	06311	05289	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5291	06313	05290	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5292	06314	05291	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5293	06315	05292	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5294	06316	05293	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5295	06317	05294	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5296	06318	05295	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5297	06319	05296	5		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5298	06320	05297	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5299	06321	05298	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5300	06322	05299	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5301	06323	05300	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5302	06324	05301	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5303	06325	05302	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5304	06326	05303	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5305	06327	05304	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5306	06329	05305	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5307	06330	05306	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5308	06331	05307	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5309	06332	05308	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5310	06333	05309	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5311	06334	05310	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5312	06335	05311	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5313	06337	05312	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	

Table 148





Table 151

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AD	AE	AF	AG	AJ	AK	AM	AO	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
5422	06454	05421	1																																
5423	06455	05422	1																																
5424	06456	05423	1																																
5425	06457	05424	1																																
5426	06458	05425	1																																
5427	06459	05426	1																																
5428	06460	05427	1																																
5429	06461	05428	1																																
5430	06462	05429	1																																
5431	06463	05430	2																																
5432	06464	05431	1																																
5433	06465	05432	1																																
5434	06466	05433	1																																
5435	06468	05434	1																																
5436	06469	05435	1																																
5437	06470	05436	1																																
5438	06471	05437	1																																
5439	06472	05438	1																																
5440	06473	05439	3																																
5441	06474	05440	1																																
5442	06475	05441	2																																
5443	06476	05442	1																																
5444	06477	05443	2																																
5445	06478	05444	1																																
5446	06481	05445	1																																
5447	06482	05446	2																																
5448	06483	05447	1																																
5449	06484	05448	1																																
5450	06485	05449	1																																
5451	06486	05450	1																																
5452	06487	05451	1																																
5453	06488	05452	2																																
5454	06489	05453	2																																
5455	06490	05454	1																																
5456	06491	05455	1																																
5457	06492	05456	2																																

Table 152



	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AI	AK	AM	AO	AS	AW	AY	BA	BC	BE	BF	BG	BI	DK
5458	06493	05457	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
5459	06496	05458	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0					
5460	06498	05459	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5461	06499	05460	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5462	06500	05461	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5463	06501	05462	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5464	06502	05463	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5465	06503	05464	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5466	06504	05465	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5467	06505	05466	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5468	06506	05467	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5469	06507	05468	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5470	06508	05469	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5471	06509	05470	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5472	06510	05471	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5473	06511	05472	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5474	06512	05473	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5475	06513	05474	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5476	06514	05475	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5477	06515	05476	4		0	0																										

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AE	AG	AI	AK	AM	AO	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
5494	06532	05493	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	
5495	06533	05494	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	
5496	06536	05495	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	
5497	06537	05496	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	
5498	06538	05497	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	
5499	06539	05498	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	
5500	06540	05499	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	
5501	06541	05500	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	
5502	06542	05501	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	
5503	06544	05502	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	
5504	06545	05503	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	
5505	06546	05504	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	
5506	06547	05505	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	
5507	06548	05506	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	
5508	06549	05507	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	
5509	06550	05508	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	
5510	06551	05509	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	
5511	06552	05510	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	
5512	06553	05511	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	
5513	06555	05512	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	
5514	06556	05513	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	
5515	06557	05514	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	
5516	06558	05515	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	
5517	06559	05516	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	
5518	06560	05517	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	
5519	06561	05518	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	
5520	06563	05519	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	
5521	06564	05520	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	
5522	06565	05521	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	
5523	06566	05522	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	
5524	06567	05523	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	
5525	06569	05524	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	
5526	06571	05525	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	
5527	06572	05526	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	
5528	06573	05527	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	
5529	06574	05528	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	

Table 154

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AI	AG	AL	AS	AT	BA	BB	BC	BE	BF	BG	BH	BI	BK
530	06576	05529	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
531	06577	05530	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
532	06578	05531	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
533	06579	05532	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
534	06580	05533	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
535	06581	05534	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
536	06582	05535	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
537	06583	05536	3	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
538	06584	05537	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
539	06585	05538	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
540	06586	05539	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
541	06587	05540	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
542	06588	05541	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
543	06590	05542	3	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
544	06592	05543	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
545	06593	05544	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
546	06594	05545	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
547	06595	05546	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
548	06596	05547	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
549	06597	05548	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
550	06599	05549	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
551	06600	05550	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
552	06601	05551	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
553	06602	05552	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
554	06603	05553	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
555	06604	05554	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
556	06605	05555	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
557	06606	05556	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
558	06607	05557	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
559	06608	05558	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
560	06609	05559	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
561	06610	05560	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
562	06611	05561	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
563	06612	05562	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
564	06613	05563	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
565	06614	05564	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Table 155

[illegible]

[illegible]



[illegible]





	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AI	AK	AM	AO	AS	AW	AY	BA	BC	BE	BF	BG	BH	BI	BK
5746	06819	05745	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5747	06820	05746	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5748	06821	05747	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5749	06823	05748	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5750	06824	05749	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5751	06825	05750	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5752	06826	05751	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5753	06827	05752	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5754	06828	05753	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5755	06829	05754	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5756	06830	05755	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5757	06831	05756	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5758	06832	05757	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5759	06833	05758	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5760	06834	05759	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5761	06835	05760	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5762	06836	05761	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5763	06837	05762	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5764	06838	05763	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5765	06839	05764	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5766	06840	05765	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5767	06841	05766	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5768	06842	05767	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5769	06843	05768	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5770	06844	05769	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5771	06845	05770	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5772	06846	05771	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5773	06848	05772	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5774	06850	05773	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5775	06851	05774	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5776	06852	05775	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5777	06854	05776	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5778	06855	05777	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5779	06856	05778	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5780	06857	05779	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5781	06858	05780	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						

Table 161

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AO	AS	AW	AY	BA	BC	BE	BF	BG	BH	BI	BK
5702	06859	05781	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
5703	06863	05782	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
5704	06864	05783	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
5705	06865	05784	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
5706	06866	05785	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
5707	06869	05786	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
5708	06870	05787	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
5709	06871	05788	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
5710	06872	05789	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
5711	06873	05790	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
5712	06874	05791	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
5713	06875	05792	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
5714	06876	05793	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
5715	06878	05794	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
5716	06879	05795	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
5717	06880	05796	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
5718	06882	05797	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
5719	06883	05798	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
5720	06884	05799	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
5721	06885	05800	2	0	0																												

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AV	AC	AF	AI	AK	AM	AO	AS	AW	AY	BA	BC	BE	BF	BG	BH	BI	BK
5818	06904	05817	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5819	06906	05818	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5820	06909	05819	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5821	06910	05820	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5822	06911	05821	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5823	06912	05822	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5824	06913	05823	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5825	06915	05824	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5826	06916	05825	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5827	06917	05826	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5828	06919	05827	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5829	06920	05828	27	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	5	22	0	0	0	0	0	0	0	0	0
5830	06922	05829	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
5831	06923	05830	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
5832	06927	05831	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						906
5833	06928	05832	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5834	06929	05833	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5835	06930	05834	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0						
5836	06931	05835	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5837	06932	05836	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						3702
5838	06933	05837	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	1	0	0	0						
5839	06934	05838	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5840	06935	05839	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5841	06936	05840	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5842	06937	05841	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5843	06938	05842	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5844	06939	05843	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5845	06941	05844	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5846	06942	05845	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5847	06943	05846	7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5848	06945	05847	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5849	06946	05848	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5850	06947	05849	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0						
5851	06948	05850	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5852	06949	05851	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0</													



	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AI	AK	AM	AQ	AS	AT	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
5890	06995	05889	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0							
5891	06996	05890	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0						
5892	06997	05891	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5893	06998	05892	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5894	06999	05893	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5895	07000	05894	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5896	07001	05895	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5897	07002	05896	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5898	07003	05897	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1	0	0	0	0					
5899	07004	05898	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0					
5900	07005	05899	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5901	07006	05900	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5902	07007	05901	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	3	0	0	0	0	0					
5903	07008	05902	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5904	07009	05903	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5905	07011	05904	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5906	07012	05905	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1	0	0					
5907	07013	05906	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5908	07014	05907	1</																															

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AI	AK	AM	AO	AS	AW	AY	BA	BC	BE	BF	BG	BH	BI	BK
5926	07034	05925	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5927	07035	05926	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5928	07036	05927	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5929	07037	05928	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5930	07038	05929	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5931	07039	05930	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5932	07040	05931	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5933	07041	05932	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5934	07043	05933	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5935	07044	05934	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5936	07046	05935	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5937	07047	05936	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5938	07048	05937	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5939	07049	05938	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5940	07050	05939	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5941	07053	05940	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5942	07054	05941	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5943	07055	05942	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5944	07056	05943	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5945	07057	05944	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5946	07058	05945	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5947	07059	05946	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5948	07060	05947	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5949	07061	05948	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5950	07062	05949	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5951	07063	05950	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5952	07065	05951	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5953	07066	05952	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5954	07067	05953	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5955	07068	05954	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5956	07069	05955	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5957	07071	05956	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5958	07072	05957	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5959	07074	05958	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5960	07075	05959	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5961	07076	05960	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AI	AK	AM	AO	AS	AW	AY	BA	BC	BE	BF	BG	BH	BI	BK
5962	07079	05961	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5963	07080	05962	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5964	07081	05963	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5965	07082	05964	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5966	07083	05965	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5967	07084	05966	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5968	07085	05967	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5969	07086	05968	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5970	07087	05969	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5971	07088	05970	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5972	07089	05971	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5973	07091	05972	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5974	07093	05973	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5975	07094	05974	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5976	07095	05975	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5977	07096	05976	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5978	07097	05977	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5979	07098	05978	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5980	07099	05979	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5981	07100	05980	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5982	07101	05981	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5983	07102	05982	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5984	07103	05983	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5985	07104	05984	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5986	07105	05985	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5987	07106	05986	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5988	07108	05987	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5989	07110	05988	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5990	07111	05989	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5991	07112	05990	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5992	07113	05991	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5993	07114	05992	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5994	07115	05993	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5995	07116	05994	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5996	07117	05995	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5997	07118	05996	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					

Table 167

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AD	AE	AF	AG	AH	AI	AJ	AK	AL	AM	AN	AO	AP	AQ	AR	AS	AT	AU	AV	AW	AX	AY	AZ	BA	BB	BC	BE	BF	BG	BH	BI	BK				
5998	07119	05997	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5999	07120	05998	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6000	07121	05999	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6001	07122	06000	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6002	07123	06001	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6003	07124	06002	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6004	07125	06003	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6005	07126	06004	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6006	07127	06005	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6007	07128	06006	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6008	07129	06007	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6009	07130	06008	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6010	07131	06009	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6011	07132	06010	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6012	07133	06011	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6013	07134	06012	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6014	07135	06013	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6015	07136	06014	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6016	07137	06015	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6017	07138	06016	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6018	07139	06017	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6019	07140	06018	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0																															

Table 168



[illegible]

[illegible]

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AI	AK	AM	AN	AO	AS	AW	AY	BA	BC	BE	BF	BG	BH	BI	BK
5	6106	07259	06105	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	6107	07261	06106	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	6108	07263	06107	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	6109	07264	06108	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	6110	07265	06109	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	6111	07266	06110	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	6112	07267	06111	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	6113	07268	06112	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	6114	07269	06113	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	6115	07270	06114	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	6116	07272	06115	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	6117	07274	06116	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	6118	07275	06117	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	6119	07276	06118	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	6120	07277	06119	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	6121	07278	06120	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	6122	07279	06121	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	6123	07280	06122	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	6124	07281	06123	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	6125	07282	06124	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	6126	07283	06125	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	6127	07284	06126	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	6128	07285	06127	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	6129	07286	06128	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	6130	07287	06129	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	6131	07288	06130	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	6132	07289	06131	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	6133	07290	06132	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	6134	07291	06133	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	6135	07292	06134	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	6136	07293	06135	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	6137	07294	06136	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	6138	07295	06137	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	6139	07296	06138	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AI	AK	AM	AO	AS	AW	AY	BA	BC	BE	BF	BG	BI	BK
50	6142	07299 06141	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
	6143	07300 06142	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
	6144	07301 06143	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
	6145	07302 06144	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
	6146	07303 06145	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
	6147	07304 06146	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
	6148	07305 06147	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
	6149	07306 06148	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
	6150	07307 06149	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
	6151	07308 06150	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
	6152	07309 06151	5		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
	6153	07311 06152	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
	6154	07312 06153	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
	6155	07313 06154	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
	6156	07315 06155	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
	6157	07316 06156	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
	6158	07317 06157	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
	6159	07318 06158	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
	6160	07319 06159	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
	6161	07320 06160	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
	6162	07321 06161	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
	6163	07322 06162	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
	6164	07323 06163	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
	6165	07324 06164	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
	6166	07325 06165	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
	6167	07326 06166	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
	6168	07327 06167	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
	6169	07328 06168	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
	6170	07329 06169	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
	6171	07330 06170	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
	6172	07331 06171	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
	6173	07332 06172	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
	6174	07333 06173	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
	6175	07334 06174	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
	6176	07335 06175	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0									

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[illegible]





	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AN	AC	AF	AG	AI	AK	AM	AQ	AS	AW	AY	BA	BC	BE	BF	BG	BH	BI	BK
6286	07447	06285	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6287	07448	06286	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6288	07449	06287	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1	0						
6289	07450	06288	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6290	07451	06289	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6291	07452	06290	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6292	07453	06291	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6293	07454	06292	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6294	07455	06293	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6295	07456	06294	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6296	07457	06295	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6297	07458	06296	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6298	07459	06297	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6299	07460	06298	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6300	07461	06299	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6301	07462	06300	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6302	07463	06301	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6303	07464	06302	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6304	07465	06303	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6305	07466	06304	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6306	07467	06305	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6307	07468	06306	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6308	07469	06307	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6309	07470	06308	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6310	07471	06309	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6311	07472	06310	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6312	07473	06311	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6313	07474	06312	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6314	07475	06313	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6315	07476	06314	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6316	07477	06315	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6317	07478	06316	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6318	07479	06317	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6319	07480	06318	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6320	07481	06319	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6321	07483	06320	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						



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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AI	AG	AK	AM	AO	AS	AW	AY	BA	BC	BE	BF	BG	BH	BI	BK
6430	07595	06429	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6431	07596	06430	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6432	07597	06431	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6433	07598	06432	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6434	07599	06433	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6435	07600	06434	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6436	07601	06435	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6437	07602	06436	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6438	07603	06437	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6439	07604	06438	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6440	07605	06439	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6441	07606	06440	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6442	07607	06441	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6443	07608	06442	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6444	07609	06443	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6445	07610	06444	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6446	07611	06445	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6447	07612	06446	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6448	07613	06447	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6449	07614	06448	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6450	07615	06449	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6451	07616	06450	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6452	07617	06451	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6453	07619	06452	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6454	07620	06453	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6455	07621	06454	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6456	07622	06455	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6457	07623	06456	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6458	07624	06457	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6459	07625	06458	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6460	07626	06459	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6461	07627	06460	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6462	07628	06461	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6463	07629	06462	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6464	07630	06463	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6465	07631	06464	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	

Table 180

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AJ	AK	AM	AQ	AS	AW	AY	BA	BC	BE	BF	BG	BI	DI	BK
6466	07632	06465	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
6467	07633	06466	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
6468	07634	06467	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1					
6469	07635	06468	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
6470	07636	06469	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
6471	07637	06470	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
6472	07638	06471	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
6473	07639	06472	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
6474	07640	06473	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
6475	07641	06474	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
6476	07642	06475	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
6477	07643	06476	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
6478	07644	06477	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
6479	07645	06478	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
6480	07646	06479	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
6481	07647	06480	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
6482	07648	06481	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
6483	07649	06482	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
6484	07650	06483	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
6485	07651	06484	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
6486	07652	06485	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
6487	07653	06486	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
6488	07655	06487	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
6489	07656	06488	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0					
6490	07657	06489	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
6491	07658	06490	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
6492	07659	06491	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
6493	07660	06492	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
6494	07661	06493	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
6495	07663	06494	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
6496	07664	06495	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
6497	07665	06496	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
6498	07666	06497	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
6499	07667	06498	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
6500	07668	06499	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
6501	07669	06500	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					



	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AO	AS	AT	AV	AW	AY	BA	BC	BE	BF	BG	BH	BI	BK
538	07709	06537	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
539	07710	06538	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
540	07711	06539	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
541	07712	06540	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
542	07713	06541	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
543	07714	06542	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
544	07715	06543	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
545	07716	06544	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
546	07717	06545	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
547	07718	06546	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
548	07719	06547	7		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
549	07720	06548	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
550	07721	06549	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
551	07722	06550	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
552	07723	06551	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
553	07724	06552	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
554	07725	06553	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
555	07726	06554	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
556	07727	06555	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
557	07728	06556	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
558	07731	06557	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
559	07734	06558	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
560	07735	06559	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
561	07736	06560	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
562	07738	06561	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
563	07739	06562	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
564	07740	06563	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
565	07741	06564	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
566	07742	06565	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
567	07743	06566	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
568	07744	06567	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
569	07745	06568	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
570	07746	06569	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
571	07748	06570	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
572	07749	06571	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
573	07750	06572	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						

Table 183

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AW	AY	BA	BC	DE	BF	BG	BH	BI	BK
6574	07751	06573	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6575	07752	06574	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6576	07753	06575	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6577	07754	06576	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6578	07755	06577	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6579	07756	06578	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6580	07757	06579	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6581	07758	06580	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6582	07759	06581	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6583	07760	06582	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6584	07761	06583	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6585	07762	06584	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6586	07763	06585	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6587	07764	06586	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6588	07765	06587	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6589	07766	06588	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6590	07768	06589	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6591	07769	06590	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6592	07770	06591	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6593	07771	06592	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6594	07773	06593	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6595	07774	06594	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6596	07775	06595	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6597	07776	06596	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6598	07777	06597	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6599	07778	06598	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6600	07779	06599	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6601	07780	06600	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6602	07781	06601	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6603	07782	06602	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6604	07783	06603	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6605	07785	06604	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6606	07786	06605	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6607	07787	06606	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6608	07788	06607	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6609	07789	06608	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						

Table 184



[illegible]

[illegible]

[illegible]



[illegible]



[illegible]

[illegible]



	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
6898	08128	06897	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
6899	08129	06898	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
6900	08130	06899	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
6901	08131	06900	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
6902	08132	06901	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
6903	08133	06902	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
6904	08134	06903	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
6905	08135	06904	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0						
6906	08136	06905	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
6907	08137	06906	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
6908	08138	06907	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
6909	08139	06908	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
6910	08140	06909	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
6911	08141	06910	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
6912	08142	06911	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
6913	08143	06912	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
6914	08144	06913	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
6915	08145	06914	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
6916	08146	06915	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0						
6917	08147	06916	1		0</																												

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AG	AK	AM	AO	AS	AW	AY	BA	BC	BE	BF	BG	BI	RI	BK
6934	08165	06933	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	94.2	103	7	2589	2691
6935	08166	06934	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0						
6936	08167	06935	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0						
6937	08168	06936	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0						
6938	08169	06937	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0						
6939	08170	06938	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0						
6940	08172	06939	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0						
6941	08173	06940	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0						
6942	08174	06941	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0						
6943	08175	06942	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0						
6944	08176	06943	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0						
6945	08177	06944	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0						
6946	08178	06945	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0						
6947	08179	06946	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0						
6948	08180	06947	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0						
6949	08181	06948	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0						
6950	08182	06949	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0						
6951	08184	06950	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0						
6952	08185	06951	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0						
6953	08186	06952	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0						
6954	08188	06953	1		0	0	0	0																							

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AI	AJ	AK	AN	AO	AS	AT	AW	AY	BABC	BE	BF	BG	BI	II	BK
6970	08204	06969	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6971	08205	06970	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6972	08206	06971	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6973	08207	06972	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6974	08208	06973	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6975	08209	06974	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6976	08210	06975	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6977	08211	06976	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6978	08212	06977	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6979	08213	06978	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6980	08214	06979	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6981	08215	06980	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6982	08216	06981	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6983	08217	06982	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6984	08218	06983	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6985	08219	06984	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6986	08220	06985	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6987	08221	06986	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6988	08222	06987	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6989	08223	06988	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6990	08224	06989	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6991	08225	06990	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6992	08226	06991	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6993	08227	06992	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6994	08228	06993	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6995	08229	06994	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6996	08230	06995	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6997	08232	06996	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6998	08233	06997	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6999	08234	06998	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7000	08235	06999	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7001	08236	07000	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7002	08237	07001	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7003	08238	07002	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7004	08239	07003	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7005	08240	07004	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						

Table 195

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AG	AI	AK	AM	AQ	AS	AW	AY	B	BC	BE	BF	BG	BI	BK
7006	08241	07005	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7007	08242	07006	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7008	08243	07007	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7009	08244	07008	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7010	08245	07009	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7011	08246	07010	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7012	08247	07011	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7013	08248	07012	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7014	08249	07013	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7015	08250	07014	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7016	08251	07015	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7017	08252	07016	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7018	08253	07017	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7019	08254	07018	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7020	08255	07019	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7021	08256	07020	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7022	08257	07021	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7023	08258	07022	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7024	08259	07023	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7025	08260	07024	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7026	08261	07025	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7027	08262	07026	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7028	08263	07027	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7029	08264	07028	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7030	08265	07029	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7031	08266	07030	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7032	08267	07031	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7033	08268	07032	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7034	08269	07033	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7035	08270	07034	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7036	08271	07035	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7037	08272	07036	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7038	08273	07037	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7039	08274	07038	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7040	08275	07039	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7041	08276	07040	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Table 196

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AI	AJ	AK	AM	AO	AS	AW	AY	BA	BB	BC	BE	BF	BG	BH	BI	BK
7042	08277	07041	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0						
7043	08278	07042	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0						
7044	08279	07043	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	2	0	0						
7045	08280	07044	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0						
7046	08281	07045	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0						
7047	08282	07046	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0						
7048	08283	07047	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0						
7049	08284	07048	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0						
7050	08285	07049	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0						
7051	08286	07050	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0						
7052	08287	07051	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0						
7053	08288	07052	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0						
7054	08289	07053	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0						
7055	08290	07054	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0						
7056	08291	07055	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0						
7057	08292	07056	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0						
7058	08293	07057	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0						
7059	08294	07058	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0						
7060	08295																																		

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AO	AS	AT	BB	BC	BE	BF	BG	BH	BI	BK
7186	08423	07185	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7187	08424	07186	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7188	08425	07187	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7189	08426	07188	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7190	08427	07189	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7191	08428	07190	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7192	08429	07191	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7193	08430	07192	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7194	08431	07193	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7195	08432	07194	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7196	08434	07195	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7197	08435	07196	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7198	08436	07197	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7199	08437	07198	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7200	08438	07199	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7201	08439	07200	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7202	08440	07201	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7203	08441	07202	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7204	08442	07203	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7205	08443	07204	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7206	08444	07205	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7207	08445	07206	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7208	08446	07207	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7209	08447	07208	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7210	08448	07209	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7211	08449	07210	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7212	08450	07211	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7213	08451	07212	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7214	08452	07213	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7215	08453	07214	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7216	08454	07215	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7217	08455	07216	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7218	08456	07217	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7219	08457	07218	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7220	08458	07219	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7221	08459	07220	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7222	08460	07221	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7223	08461	07222	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7224	08462	07223	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7225	08463	07224	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7226	08464	07225	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7227	08465	07226	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7228	08466	07227	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7229	08467	07228	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7230	08468	07229	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7231	08469	07230	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7232	08470	07231	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7233	08471	07232	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7234	08472	07233	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7235	08473	07234	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7236	08474	07235	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7237	08475	07236	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7238	08476	07237	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7239	08477	07238	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7240	08478	07239	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7241	08479	07240	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7242	08480	07241	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7243	08481	07242	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0</									

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AJ	AK	AM	AO	AS	AW	AY	BABC	BE	BF	BG	BH	BI	BK
7294	08532	07293	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7295	08533	07294	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7296	08534	07295	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7297	08535	07296	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7298	08536	07297	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7299	08537	07298	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7300	08538	07299	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7301	08539	07300	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7302	08540	07301	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7303	08541	07302	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7304	08542	07303	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7305	08543	07304	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7306	08544	07305	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7307	08545	07306	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7308	08546	07307	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7309	08547	07308	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	06633	95.2	310	1	1124	1724
7310	08548	07309	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7311	08549	07310	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7312	08550	07311	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7313	08551	07312	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7314	08552	07313	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7315	08553	07314	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7316	08554	07315	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7317	08555	07316	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7318	08556	07317	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7319	08557	07318	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7320	08558	07319	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7321	08559	07320	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7322	08560	07321	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7323	08561	07322	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7324	08563	07323	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7325	08564	07324	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7326	08565	07325	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7327	08566	07326	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7328	08567	07327	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0									

Table 204

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AG	AI	AK	AM	AQ	AS	AV	AW	AY	BABC	BE	BF	BGBH	BI	BK
7330	08569	07329	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7331	08570	07330	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7332	08571	07331	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7333	08572	07332	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7334	08573	07333	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7335	08574	07334	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7336	08575	07335	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7337	08576	07336	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7338	08577	07337	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7339	08578	07338	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7340	08579	07339	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7341	08580	07340	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7342	08581	07341	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7343	08582	07342	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7344	08583	07343	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7345	08584	07344	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7346	08585	07345	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7347	08586	07346	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7348	08587	07347	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7349	08588	07348	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7350	08589	07349	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7351	08591	07350	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7352	08592	07351	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7353	08593	07352	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7354	08594	07353	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7355	08595	07354	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7356	08596	07355	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7357	08597	07356	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7358	08598	07357	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7359	08599	07358	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7360	08600	07359	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7361	08601	07360	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7362	08602	07361	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7363	08603	07362	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7364	08604	07363	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7365	08605	07364	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
																								</							

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AW	AY	BA	BC	BE	BF	BG	BH	BI	BK
7366	08606	07365	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7367	08607	07366	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7368	08608	07367	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7369	08609	07368	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7370	08610	07369	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7371	08611	07370	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7372	08612	07371	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7373	08613	07372	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7374	08614	07373	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7375	08615	07374	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7376	08616	07375	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7377	08617	07376	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7378	08618	07377	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7379	08619	07378	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7380	08620	07379	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7381	08621	07380	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7382	08622	07381	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7383	08623	07382	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7384	08624	07383	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7385	08625	07384	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7386	08626	07385	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7387	08627	07386	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7388	08628	07387	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7389	08629	07388	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7390	08630	07389	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7391	08631	07390	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7392	08632	07391	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7393	08633	07392	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7394	08634	07393	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7395	08635	07394	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7396	08636	07395	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7397	08637	07396	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7398	08638	07397	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7399	08639	07398	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7400	08640	07399	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7401	08641	07400	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						

Table 207.

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AD	AG	AI	AK	AM	AO	AS	AW	AY	BABC	BE	BF	BG	BH	BI	BK	
7430	08679	07437	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	102426	98.6	360	1	1209	1599
7439	08680	07438	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	94.7	266	1	2220	2484
7440	08681	07439	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7441	08682	07440	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7442	08683	07441	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7443	08684	07442	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7444	08685	07443	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7445	08686	07444	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7446	08687	07445	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7447	08688	07446	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7448	08689	07447	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7449	08690	07448	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7450	08691	07449	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7451	08692	07450	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7452	08693	07451	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7453	08694	07452	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7454	08695	07453	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7455	08696	07454	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7456	08697	07455	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7457	08698	07456	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7458	08699	07457	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7459	08700	07458	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7460	08701	07459	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7461	08702	07460	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7462	08703	07461	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7463	08704	07462	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7464	08705	07463	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7465	08706	07464	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7466	08707	07465	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7467	08708	07466	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7468	08709	07467	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7469	08710	07468	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7470	08711	07469	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7471	08712	07470	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7472	08713	07471	1		0	0	0	0	0	0	0	0	0	0	0	0</																	



Table 209

[illegible]

[illegible]

[illegible]

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AV	AW	AY	BA	BC	BE	BF	BG	BI	BI	BK
7618	08864	07617	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	X68742	94.1	101	1	263	3453
7619	08865	07618	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7620	08866	07619	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7621	08867	07620	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7622	08868	07621	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7623	08869	07622	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7624	08870	07623	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7625	08871	07624	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7626	08872	07625	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7627	08873	07626	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7628	08874	07627	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7629	08875	07628	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7630	08876	07629	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7631	08877	07630	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7632	08878	07631	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7633	08879	07632	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7634	08880	07633	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7635	08881	07634	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7636	08882	07635	1																															

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AE	AG	AI	AK	AM	AQ	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
7654	08900	07653	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7655	08901	07654	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7656	08902	07655	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7657	08903	07656	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7658	08904	07657	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7659	08905	07658	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7660	08906	07659	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7661	08908	07660	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7662	08909	07661	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7663	08910	07662	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7664	08912	07663	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7665	08913	07664	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7666	08914	07665	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7667	08915	07666	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7668	08916	07667	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7669	08917	07668	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7670	08919	07669	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7671	08920	07670	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7672	08921	07671	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7673	08922	07672	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7674	08923	07673	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7675	08924	07674	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7676	08925	07675	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7677	08926	07676	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7678	08927	07677	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7679	08928	07678	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7680	08929	07679	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7681	08930	07680	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7682	08931	07681	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7683	08932	07682	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7684	08933	07683	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7685	08934	07684	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7686	08935	07685	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7687	08936	07686	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7688	08937	07687	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7689	08938	07688	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						

Table 214

[illegible]

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AI	AK	AM	AO	AS	AW	AY	BABC	BE	BF	BG	BH	BI	BK		
7726	08975	07725	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0							
7727	08976	07726	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7728	08977	07727	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7729	08978	07728	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7730	08979	07729	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7731	08980	07730	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7732	08981	07731	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7733	08982	07732	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7734	08983	07733	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7735	08984	07734	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7736	08985	07735	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7737	08986	07736	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7738	08987	07737	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	014695	95.5	359	1	1316	1860
7739	08988	07738	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0							
7740	08989	07739	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0							
7741	08990	07740	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0							
7742	08991	07741	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0							
7743	08992	07742	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0							
7744	08993	07743	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0							
7745	08994	07744	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0							
7746	08995	07745	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0							
7747	08996	07746	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0							
7748	08997	07747	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0							
7749	08998	07748	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0							
7750	08999	07749	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0							
7751	09000	07750	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0							
7752	09001	07751	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0							
7753	09002	07752	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0							
7754	09003	07753	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0							
7755	09004	07754	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0							
7756	09005	07755	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0							
7757	09006	07756	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0							
7758	09007	07757	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0							
7759	09008	07758	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0							
7760	09009	07759	1		0	0	0	0	0	0	0	0	0	0	0	0																		



	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AI	AK	AM	AO	AS	AW	AY	BA	BC	BE	BF	BG	BH	BI	BK
7762	09011	07761	1																														
7763	09012	07762	1																														
7764	09013	07763	1																														
7765	09014	07764	2																														
7766	09015	07765	1																														
7767	09016	07766	1																														
7768	09017	07767	1																														
7769	09018	07768	1																														
7770	09019	07769	1																														
7771	09020	07770	1																														
7772	09021	07771	1																														
7773	09022	07772	1																														
7774	09023	07773	1																														
7775	09024	07774	1																														
7776	09025	07775	1																														
7777	09026	07776	1																														
7778	09027	07777	1																														
7779	09028	07778	1																														
7780	09029	07779	1																														
7781	09030	07780	1																														
7782	09031	07781	1																														
7783	09032	07782	1																														
7784	09033	07783	1																														
7785	09034	07784	1																														
7786	09035	07785	1																														
7787	09036	07786	2																														
7788	09037	07787	1																														
7789	09038	07788	1																														
7790	09039	07789	2																														
7791	09040	07790	2																														
7792	09041	07791	1																														
7793	09042	07792	2																														
7794	09043	07793	1																														
7795	09044	07794	1																														
7796	09045	07795	1																														
7797	09046	07796	1																														



	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AO	AS	AW	AY	BABC	BE	BF	BGBI	BI	BK
7834	09083	07833	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1					
7835	09084	07834	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1					
7836	09085	07835	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	X56976	92 287	1	3066	3419
7837	09086	07836	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1					
7838	09087	07837	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1					



EP 0 679 716 A1

CTCCAGCCAG GGGAGCAGGG AAGAAGAAGG GGCTCCCTCC TCTTCACATT CCCCCCGACC 180  
 CCAAAGCCAG AGAAAGCCAG ATGGCACCAG CTGCTCCGGA TGTGCCTGCC CACATTGGGG 240  
 GACAGGGCCG GGCCTGGGCT CGGTTCCNAG GTTTGAGCTC TGCAGNCTGT GTCCTGGNGT 300  
 5 GAGGGGGCTG AAGTNAGNCC AAAGGAAGAA CTNAGTN 337

SEQ ID NO:5247  
 SEQUENCE LENGTH:168  
 SEQUENCE TYPE:nucleic acid  
 10 TOPOLOGY:linear  
 CLONE:HUMGS06262  
 SEQUENCE DESCRIPTION:  
 GATCACCTNA TTTTNAAC AAAATATTN TAACAGGAAT GGGTGGGAGT NCTGGTGAAA 60  
 15 AGAGGTGAAA TGTGGTTGTA TGAGCCAATC ATATTGTAA TTNTTAAAA AAAGTTTAAA 120  
 AGGAAATATC TGTCTGAAA CCCCACTTAA GCATTGTNTT NNTATAAN 168

SEQ ID NO:5248  
 SEQUENCE LENGTH:378  
 SEQUENCE TYPE:nucleic acid  
 20 TOPOLOGY:linear  
 CLONE:HUMGS06264  
 SEQUENCE DESCRIPTION:  
 25 GATCAACAAA GAGGACTTTG TGGCACTGGA GAGGCTTACC CAGGGGATGG ACATTCACTG 60  
 GATGCATGTT NCTGGTCATT CGGGATTTAT AGGCAATGAA GAAGCTGACA GATTAGCCAG 120  
 AGAAGGAGCT AAACAATCGG AAGACTGAGC CATGTGACTT TAGTCCTTNG GAGAACTTNA 180  
 GCCAGCGGCT GTCTTGCTGC CTGTACTTAC TTGTGTGGAA AATAGCCTGC AGGTAGGACC 240  
 ATTGCAGTGA TGGGCAGATT GGGTCTTTCA CACGGNGTCA GGCACAGTGG CTTTCTGTNG 300  
 30 NCATGGTNGT TTTATANANA AATNGGTAA GGTATATAAA TAAAGTNTGG NCCANCTTTT 360  
 GNNAAGGNAN GANATGGN 378

SEQ ID NO:5249  
 SEQUENCE LENGTH:131  
 SEQUENCE TYPE:nucleic acid  
 35 TOPOLOGY:linear  
 CLONE:HUMGS06267  
 SEQUENCE DESCRIPTION:  
 40 GATCANCTAC AGGAAAAGTA AATGTGAACG CAAGCAGAAT GAAACACAGT AAAAGCCGGT 60  
 CTAGCCTGCC TGGCCACACT CTCAGCGCCT TGTGAGGATG GGNCANTANA TAAANTCATC 120  
 TTTAGTAGAA A 131

SEQ ID NO:5250  
 SEQUENCE LENGTH:322  
 SEQUENCE TYPE:nucleic acid  
 45 TOPOLOGY:linear  
 CLONE:HUMGS06268  
 SEQUENCE DESCRIPTION:  
 50

55



5 SEQ ID NO:7844  
 SEQUENCE LENGTH:37  
 SEQUENCE TYPE:nucleic acid  
 STRANDEDNESS:single  
 TOPOLOGY:linear  
 SEQUENCE DESCRIPTION:  
 CTCGCTCGCC CATCCTTATA CAGGCTCAGT TTTGTCT 37

10 SEQ ID NO:7845  
 SEQUENCE LENGTH:37  
 SEQUENCE TYPE:nucleic acid  
 STRANDEDNESS:single  
 15 TOPOLOGY:linear  
 SEQUENCE DESCRIPTION:  
 CTCGCTCGCC CATGTATAGG GACAGCATTT CTGAGAG 37

20 SEQ ID NO:7846  
 SEQUENCE LENGTH:38  
 SEQUENCE TYPE:nucleic acid  
 STRANDEDNESS:single  
 TOPOLOGY:linear  
 25 SEQUENCE DESCRIPTION:  
 CTGGTTCGGC CCACCTCTGA AGGTTCCAGA ATCGATAG 38

30 SEQ ID NO:7847  
 SEQUENCE LENGTH:22  
 SEQUENCE TYPE:nucleic acid  
 STRANDEDNESS:single  
 35 TOPOLOGY:linear  
 SEQUENCE DESCRIPTION:  
 CCAGGGTTTT CCCAGTCACG AC 22

40 SEQ ID NO:7848  
 SEQUENCE LENGTH:22  
 SEQUENCE TYPE:nucleic acid  
 STRANDEDNESS:single  
 TOPOLOGY:linear  
 45 SEQUENCE DESCRIPTION:  
 TCACACAGGA AACAGCTATG AC 22

## 50 Claims

1. A purified single-stranded DNA, a purified single-stranded DNA complementary thereto, or a purified double-stranded DNA consisting of said single strands, containing all or a portion of a single-stranded DNA or a single-stranded DNA complementary thereto comprising any of the base sequences listed under SEQ ID NO 1-7837 and hybridizing specifically to a particular site of human genomic DNA, human cDNA or human mRNA.





2. A DNA probe consisting of a purified single-stranded DNA , a purified single-stranded DNA complementary thereto, or a purified double-stranded DNA consisting of said single strands, containing all or a portion of a single-stranded DNA or a single-stranded DNA complementary thereto comprising any of the base sequences listed under SEQ ID NO 1-7837 and hybridizing specifically to a particular site of human genomic DNA, human cDNA or human mRNA.
3. A DNA primer consisting of a purified single-stranded DNA, a purified single-stranded DNA complementary thereto, or a purified double-stranded DNA consisting of said single strands, containing all or a portion of a single-stranded DNA or a single-stranded DNA complementary thereto comprising any of the base sequences listed under SEQ ID NO 1-7837 and hybridizing specifically to a particular site of human genomic DNA, human cDNA or human mRNA.
4. A purified single-stranded DNA, a purified single-stranded DNA complementary thereto, or a purified double-stranded DNA consisting of said single strands, containing all or a portion of a single-stranded DNA or a single-stranded DNA complementary thereto, wherein said single-stranded DNA is complementary to a human mRNA containing any of the base sequences listed under SEQ ID NO 1-7837 (wherein T is read as U) or any portion thereof at its 3' region, and hybridizing specifically to a particular site of human genomic DNA, human cDNA or human mRNA.
5. A DNA probe consisting of a purified single-stranded DNA, a purified single-stranded DNA complementary thereto, or a purified double-stranded DNA consisting of said single strands, containing all or a portion of a single-stranded DNA or a single-stranded DNA complementary thereto, wherein said single-stranded DNA is complementary to a human mRNA containing any of the base sequences listed under SEQ ID NO 1-7837 (wherein T is read as U) or any portion thereof at its 3' region, and hybridizing specifically to a particular site of human genomic DNA, human cDNA or human mRNA.
6. A DNA primer consisting of a purified single-stranded DNA, a purified single-stranded DNA complementary thereto, or a purified double-stranded DNA consisting of said single strands, containing all or a portion of a single-stranded DNA or a single-stranded DNA complementary thereto, wherein said single-stranded DNA is complementary to a human mRNA containing any of the base sequences listed under SEQ ID NO 1-7837 (wherein T is read as U) or any portion thereof at its 3' region, and hybridizing specifically to a particular site of human genomic DNA, human cDNA or human mRNA.



Fig. 1

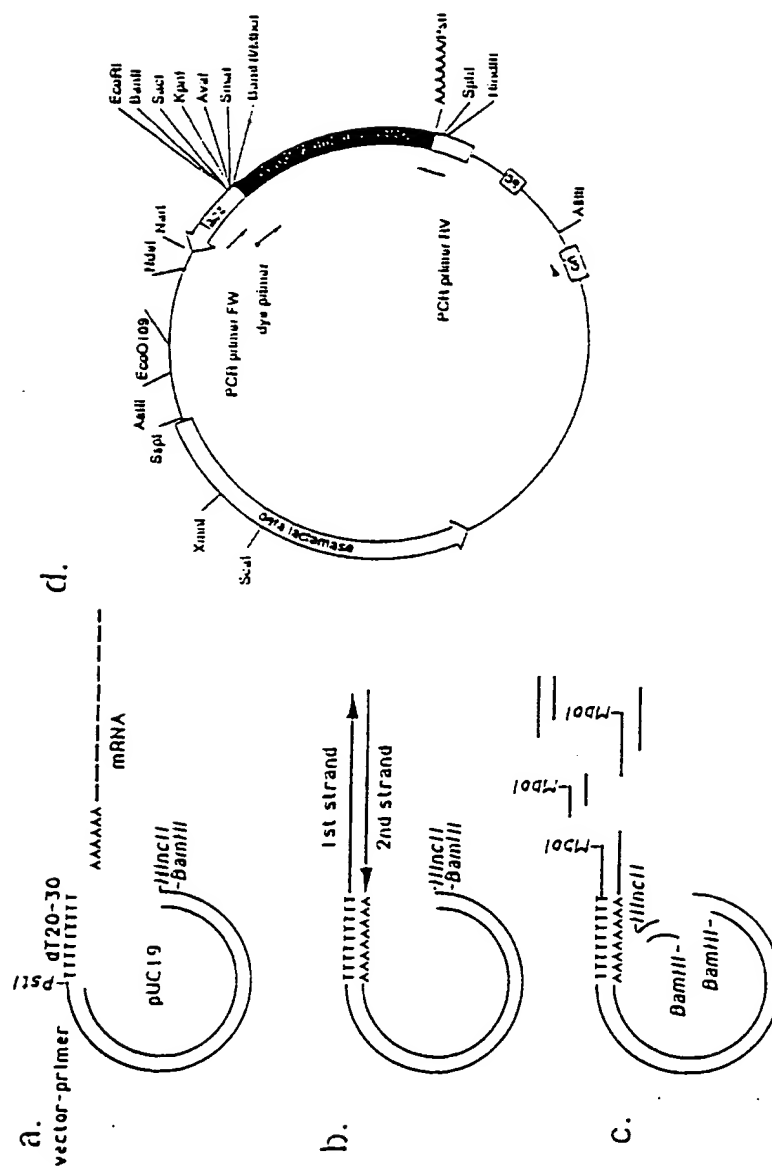




Fig. 2





Fig. 3

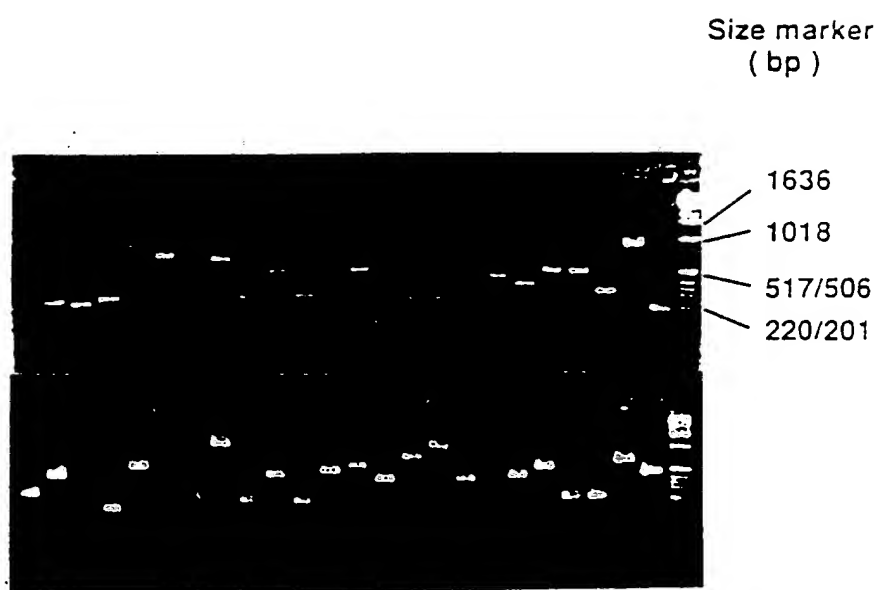






Fig. 4

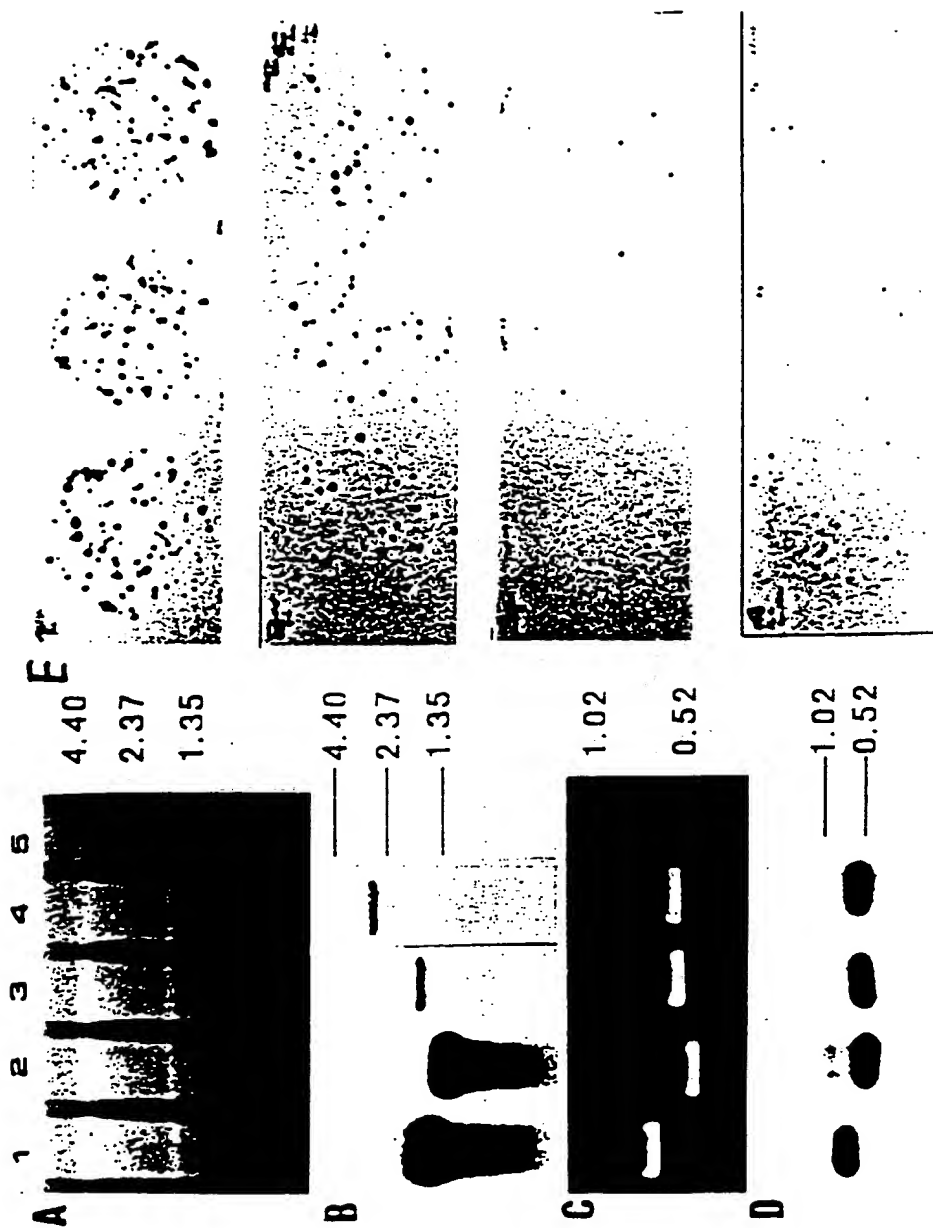




Fig. 4

F

probe No.	1	2	3	4
gene	Elongation factor 1- $\alpha$	$\alpha$ 1-antitrypsin	HnRNP core protein A1	Inter- $\alpha$ -trypsin inhibitor
(a) Band intensity of Northern blot(cpm)	687	423	10	15
(b) Band intensity of control blot(cpm)	133	177	100	127
(c) Normalized signal(a)/(b)x10	52	24	1	1.2
(d) Positive signals on colony blot	307	119	7	9
(e) Relative representation	44	17	1	1.3



Fig. 5

Appearance frequencies of various cDNAs in the 3'-directed HepG2 cDNA library

Group	Clone	Gene	A in 982 (%)	B "in 8,800 (%)"	C "in 26,400 (%)"
I	a15	Elongation factor - 1A $\alpha$	22 (2.2)	307 (3.5)	NT
	c321	Translationally restricted tumor protein	12 (1.2)	89 (1.0)	NT
	lb038	$\alpha$ -1-antitrypsin	8 (0.8)	119 (1.4)	NT
	hm01b02	Light chain of ferritin	6 (0.6)	62 (0.7)	NT
	c13a04	NADP(H) Menadione oxidoreductase	4 (0.4)	27 (0.3)	NT
	hm02d02	Ribosomal protein S11	3 (0.3)	29 (0.3)	NT
	lb042	Human RNP core protein A1	2 (0.2)	7 (0.1)	NT
	s155	unknown	1	2	5 (0.02)
II	s159	unknown	1	2	4 (0.02)
	s639	unknown	1	1	3 (0.01)
	s635	unknown	1	0	2 (0.01)
	s170	unknown	1	0	1 (0.004)
	s154	unknown	1	0	1 (0.004)
	s167	unknown	1	0	1 (0.004)
	s645	unknown	1	0	1 (0.004)
	s647	unknown	1	0	0 (<0.004)
	s632	unknown	1	0	0 (<0.004)



Fig. 6

Sequences of primers											
GS	Ctl	Chromosomal position	Sense	Anti-sense	AT	HP	HE	HO	CO	G	T
91001708	pm2366	1	CAGAGCCAGTACAACTAT	AAGTTATGTGGGTCAG	48	114	115	104	110	1	2
91001026	pm2444	1	AATGGACAGTTACACTGA	CCAGCTCCTTGACTTGAGA	48	83	81	>200	>200	1	1
91001075	pm0883	1	TGAGCTGTGATACCTATCT	ACAAGTACCCCTGATGGCT	48	124	124	103	107	4	4
91001067	pm1772	1	GTACCTTCAGCCATAGCAC	ACCATCTCAGCCCACTTT	50	104	104	180	>200	6	6
91001094	pm0347	1	GCCTTACACAGGAACTC	TAATTCCTCCAGTCCGTAAC	51	114	116	>200	200	1	1
91001116	pm1771	1	GGGTTTCAATAGGCTGTAGACC	GCCCAATCTGTCAAACTG	49	95	95	78	107	1	1
91001191	pm0609	1	TTGCTGGATTGTAACTTTG	GGCTGAACATTCACCTTTG	47	87	87	-	200	1	1
91001200	pm1251	1	TTAGAGAGACCTTATGGAGACC	AATATCTGTGTGATGACATTAC	47	97	98	-	-	1	1
91001246	pm0982	1	TCAGGTCTGCTGGAGGATG	AATACAGACAGTATTTG	53	120	122	>200	>200	1	1
91001446	pm1518	1	AAGGTGTACAGGATTTGGCAGA	TGCAATAGCCCAATCTCAT	47	130	125	>200	>200	1	1
91001464	pm1439	1	CCAAAGCTCCGTTGAACA	TTGGGAGAGCCATAGACAG	51	100	100	>200	-	1	1
91001468	pm0227	1	TACTAGTGGMAAGATAAAC	CAGTGGACCAATTTCTTA	40	98	98	-	-	2	2
91001521	pm2785	1	CCCAATCAATTTGTAATG	TTGCAATCAGAGACATGAAGTT	43	102,175	100	>200	>200	1	1
91001554	pm2291	1	CCAGAGAGTCAAGGATG	GGTACAAAGTGCMAATGACT	46	57	57	78	155	1	1
91001572	pm2006	1	CCACATGTGCTAGCACGTG	AACTTTATGGAGCTCTT	44	58	58	>200	>200	4	4
91001626	pm1720	2	CATGACTCTTGGTGGTA	AACAGTAGTGGCAGCAT	46	84	109	-	-	1	1
91001036	pm0931	2	AGGTGATTTGCTCTAATA	CCGGTTATGCTACATGCT	48	119	119	93	115	1	1
91001050	pm0925	2	AAAGCAATACAAATACCAA	TTCAATATGTTTAAACAGTA	40	90	50	-	-	1	1
91001213	pm2010	2	TAATGACACCATGATAG	TAATGTAATAGCAGTTAA	45	88	88	-	-	1	1
91001268	pm0935	2	CCAGATGGAAGGGAAGTCT	CTGGAAATGGAGAAATCAACAG	47	125	125	150	>200	1	1
91001438	pm2435	2	TGGAGTTTGTCTCTAATA	GGAAATATCGCTTCAGTTG	43	103	103	-	-	1	1
91001442	pm1671	2	ATGCTCTTGGCTCCTCAT	TATGCTAGTGGCTTTATG	52	137	137	>200	-	1	1
91001453	pm1245	2	TTATAGGAGATCATTTCTGTG	ATCCGTGCCACACATAGTA	45	105	108	-	-	1	2
91001453	pm1245	2	TTGCTTCCCGCTCTAAGT	AGTCCCATCTGCCACATG	45	67	65	>200	>200	1	2
91001435	pm1246	2	ATCTACTTTTGTGAAAGTG	ATGTACAATTGGCTATGTAGG	45	75	75	170	190	1	1
91000875	pm0449	3	CGAACATTCACCTCTCAT	ACTGATTTGGTCCCATCTG	44	68	67	-	-	1	1
91001001	pm1758	3	TCTGGCTCTTGGTGTGGA	ATGATTTATAGGCAAGAA	43	68	65	-	-	3	6
91001218	pm2434	3	AAGAAGACACACTGCCTAA	GGCCACAGTACATATGTC	51	115	115	-	-	1	1
91001219	pm0668	3	GTAGTCTCCGCTTTAGC	ATGTATAGCAAAATCCAAAG	42	90	90	-	-	1	1
91001277	pm1729	3	GGTCTGTTATTTGACAT	AAGGATTTGATTTCTACAT	43	77	77	-	-	1	1
91001306	pm1022	3	GATCCTTGGTGTAGTTCAGTC	AACCAAGAGGATGTTTCAGA	43	75	75	155	>200	1	1
91001418	pm2209	3	ATCCAGTCCCAATCCAGT	CTGCAAAATACAGGGAATCAT	46	83	83	160	140	1	1
91001426	pm2455	3	CTCTAGCTGCTGTAGTAT	ACACGCCCCAGCCCTTACT	55	105	105	>200	>200	1	1
91002271	pm1252	4	GTCCTTTGCTATCTGTGTA	TTAAAGAGTGAATTTATTTGT	42	130	130	190	>200	1	1
				AAGCATTTATTTGAGGTTTA	43	90	90	95	>200	1	3





Fig. 7

g1000448	pm2256	4	GGCCAAGTTTCTCTAGTAT	GTTCAAGTTTATTCAGAGCA	42	62	62	62	62	69	1	2
g1001052	pm1151	4	GTCCATGCACTGTGTAT	GTCAATATTCATCATCA	43	80	80	80	80	-	1	1
g1001215	pm0988	4	AGAAATTATAGCATAGGT	TAGAGTCAMGTGGCTGTG	43	100	100	100	100	130	1	1
g1001298	pm2367	4	ATCAAGTTTATTTGCTTCA	CATCCATCATACAAAGTC	43	116	116	116	116	>200	1	1
g1000993	pm0201	5	TCTCGTGAAGAGCAGCAAA	TCTAAGGAAGAACAGCATC	49	101	102	113	200	180	1	1
g1000588	pm1889	5	AAGCAATGCCCTTCCACAG	CTAAGAGCTTGACCCCTTCAT	45	87	87	>200	>200	>200	1	1
g1001085	pm0319	5	TCACCCAGATAATTACAGT	GATACATAGCAGGTAGAT	44	120	120	-	-	-	1	1
g1001101	pm2364	5	TTACCTACCCGTGCTTTAC	AGACAATATCCAAAAGGC	47	89	89	100	>200	>200	1	1
g1001160	pm1160	5	ATTTGTGAGTGGTTACTA	AGAAATGGATGCTTTATTC	43	101	99	>200	>200	>200	1	1
g1000353	pm2720	6	AATGTATAGTCTGCTTCA	TGCATCTTCATGTCTTCT	44	78	78	72	>200	2	2	2
g1001326	pm1154	6	CATTGACAGCAGCAACAG	CTGGCCCTCTCTCTAGTA	53	102	104	145	200	1	1	1
g1001434	pm1216	6	TAGGCAAAACAGGAGAGAG	AAGGAGCTGGTGCAGGTTC	48	65	65	110	>200	1	1	1
g1001457	pm1785	6	TATATGCAATATCCAAAGTCG	TCTAATATCTGGTCCCTTATCT	46	90, >200	90	>200	>200	1	1	1
g1001523	pm0285	6	TTGTACGCTGTGCTCAGT	TTTAAATGTCATGGTAT	42	86	70	>200	100	1	1	1
g1001525	pm0328	6	GCACCTTAGCCCTCCCAAGT	TTTATATCAGTCCAGAGC	49	138	138	>200	>200	1	1	1
g1001562	pm2610	6	TCTGCTAATGACAGGACAC	TTTGAGATTTATGAGTCATTC	43	62	62	>200	45	1	1	1
g1000824	pm0991	7	GACCTAAGTGTGAATGAGT	AACCTAGCTTATGGGAATT	45	119	119	>200	-	1	2	2
g1001145	pm0281	7	AGCCAACTCGGGTCACTCT	CCAGGGAGAGGTGAGTCAT	56	159	155	115	>200	4	4	4
g1001469	pm0219	7	AATCATTTGGCGAGACTGTA	AAGACACTTATCCABACA	45	88	89	130	-	1	1	1
g1001579	pm1102	7	TCAGGCAGTCTGCTCAGATA	TTTGACAGTTAATCTGTTTA	44	77	76	170	-	1	1	1
g1001207	pm0956	8	AACAGTATGGCTGTGACAGTAG	TCCATTATAGGCCAGTCTTCAG	47	81	81	105	70	1	1	1
g1001176	pm2527	9	TTGCCCTCTAATGGTGTCTAC	AAAACCAACACACACTAG	48	99	99	118	180	1	1	1
g1001248	pm12708	9	TGTATTCGATTTGGATTCTC	CAMAGCAAAACAGCAGATA	44	95	95	-	85	1	1	1
g1000995	pm0959	97	TTGCAATCAGCCTCATTCG	CACATGCTTATGGACACT	43	55	55	-	-	1	1	1
g1001157	pm0547	97	TTAAGATCAGCCTCATTCG	AGAAAACACTGCCCTGTGG	44	74	74	72	73	1	1	1
g1001284	pm2245	10	AAGTATGTGCAAGAGTGA	GCATGCTTCCATATCAGT	45	138	139	>200	>200	2	2	2
g1000224	pm2664	10	TGTAAATGCTATCTCTCT	GCATGCTTCCATATCAGT	47	100	100	200	>200	1	1	1
g1001199	pm2664	11	ATCAAAACAAACATCCAGA	ACTATATATCTGCCAAT	42	117	121	134	95	2	2	2
g1001315	pm0880	11	GAATAGCTTGGAGATTTCAC	GGAGATCATACCTTCAGCA	46	100	100	84	95	1	1	1
g1001352	pm0145	11	AAAGTGACCTTGATGGACAGTGG	TGGAGCAAAATACATCTGACT	50	153	153	>200	160	1	2	2
g1001469	pm2943	11	AGGCTGCAAGGTAATTTACG	CACATCATGGTGAAGAGCTA	47	83	83	-	-	2	2	2
g1001570	pm0559	11	AACCTCTAGTAAGGCATTG	TTATTAAACCAATCCAGTA	37	47	47	125	53	1	1	1
g1000279	pm0268	12	CTGTAAGGTTTTGGAAATATGT	TTTCATTTTCTACAGATTATTT	42	75, 82	75	145	>200	3	3	3
g1001163	pm2756	12	AGTGATGGAAGACCTTGAG	GTTCATGTAAACGGGTGAGC	48	130	130	103	>200	1	2	2
g1001193	pm1193	12	TCTCCTAATCACACCCAGT	AATGATTCGTAGGATAGCA	49	88	88	>200	120	1	2	2
g1001235	pm1290	12	CACATGTAAGAAATCATCA	ACCTAATTTAGTTTCTCAC	46	100	100	-	-	1	1	1
g1001274	pm12790	12	CATCATGGTACAGTCAGAG	CAGTTGTCAAAATGTAATG	44	83	82	91	87	1	1	1
g1001308	pm1355	12	AGATGTGATGATCTCTCATGG	GAGACAGCAGTAAGACACAC	47	87	87	>200	>200	1	1	1
g1000159	pm0368	12	CCAAAGTCTAGGGTTACAG	TTCAATAGCCTTGGTTTAC	47	95, 165	95	>200	>200	1	1	1
	pm2645	13	CTAAGATTAATGGGATTC	AGTTAGTGTATGGCAGAGGA	46	104	104	>200	-	1	2	2



Fig. 8

91001044	pm1659	13	TTGTAAAGCCTATCAGAGTCA	AGAGAGCTATGCCATCTA	44	109,200	109	>200	100	1	1
91001200	pm1731	13	GCCTCTCCCTGCTGCTGGT	GCAGTTACATGGCTATCTCC	50	122	122	>200	190	1	1
91001352	pm0118	13	ACTGAATGGACATAGTCT	TACATTACATGATGTGA	40	61	61	95	103	1	1
91001366	pm0364	13	TGCTTAGCTTCCCTCCTTA	GAGCATTTCTGTTGCTGA	45	67	67	-	-	1	1
91001389	pm2301	13	CATGAACCTGCTCAGACAA	GCCTTACTTAAATGCTGACC	51	100	100	100, >200	-	1	1
91001492	pm0541	13	AAATGAATTAATAGCACT	ATTAGTTTACAGGGAGAAAT	41	72	72	-	74	1	1
91001367	pm0441	14	GTTTAAAGTTTGAATTTGGG	CATCCACCTTACATTTCT	41	77	77	>200	180	3	4
91001564	pm2307	14	CGTCTCAACTGCAATC	AATGCTCAITTAATCTCAAG	42	55	55	>200	>200	1	1
91001576	pm2019	14	ATCAAAATACCTTTAGTTG	ACGATAACTTTATGGAGAT	39	69	69	-	-	1	1
91001339	pm2220	15	TCCCATCTCAGTTGAAGT	TGAGAACAAAGGAACCACT	47	70	70	80	150	1	1
91000980	pm0985	16	TCCCATCTCAGTTGAAGT	ACTATGGTGGCTGAATGG	48	79	79	65	70	2	2
91001242	pm1127	16	CCCTGTGTTTACATGTCA	TATTAATCTCCCAATCAT	44	105	105	103	102	2	2
91001516	pm2543	16	ACAGTGTAAATCAAGGTG	TCTGACACTCAAGGTGCAAT	45	70	70	>200	-	1	1
91001566	pm0912	16	TTTGTGCGACTATGTAAT	TCAGTTTAAATGGGAACCAAG	41	53	53	>200	>200	1	1
91000806	pm1157	17	CTCTCCATGTTCTTACAAAG	TAGAGGAGAACTGTGGTT	47	77	77	140	>200	2	3
91001015	pm2369	17	ATATCACCCTGCCATCCAT	TCAATACGTCCTCTCAAGC	50	80	80	>200	>200	1	1
91001156	pm0202	17	CAGAAATTAAGTGCAGCAAT	TGATATCGCATCTTTAAGT	45	103	100	>200	>200	2	2
91001173	pm2117	17	AAATCTGTGGTAAATTC	GTGATCTGCTGCTACATTC	41	118	118	145	200	1	1
91001301	pm1878	17	TAAATCTGTGGAAATCTCTGGA	ACACATITGGGTTGCTTAAAG	47	100	100	95	97	1	1
91001316	pm0511	17	TGTGACAGCAGCAGCTTCAT	TGCTACATTTTAAATTCACCC	45	128	128	-	-	1	1
91001356	pm0538	17	CATCTCACAGACAGGAAC	ACCTAAGAGTCCAGAGAAAC	48	90	90	60	>200	1	1
91001495	pm2212	17	TGACTGCAATAAGGAGTTGT	GAACATACCAGCTTTATTTCT	46	90	90	180	>200	1	1
91001522	pm0642	17	GTCTCAGCAGATTTCAGGT	ACTTCTCTCTGAGACACA	45	68	68	160	-	1	1
91001078	pm1815	19	TGTTTCTCCAGCTTTGTAG	GTACATGCCCTTGGTACAG	48	65	65	>200	>200	1	1
91001417	pm0289	19	GGATCAGACCAACAGTGTCTG	GCAGGTATAAACAGATTA	46	50	50	-	-	1	1
91001467	pm1608	19	GAAGCCACCTCTGCACCTCA	GGAGGTATGGGGAACGGT	54	93	93	>200	>200	2	2
91001069	pm1879	20	GCCATGCTGTAAAGTGATGT	TTAAGAGCCATAGCTAGGATA	40	140	140	-	-	1	1
91001088	pm1146	20	CCCCTTAGGATTCACGTCTC	ACCACCCAAAGTCTTTACGG	52	66	66	180	>200	1	1
9100112	pm0112	20	TGCTGGATGACTTCACAGG	TCCCTATCAGGCTGCTGTT	49	59	59	59, 115	59	1	1
9100332	pm0332	20	CTGCTGGCTAGTCTGACTC	CAATGGTCTAAGAGGACAT	40	135	135	153	160	1	1
9100152	pm0647	20	TCTGAATGATGATGGAACA	ATCCTAGTCCCAACCCACTC	48	109	109	-	-	1	1
91001158	pm1774	20	GGAGCCACATGGATTGATTG	AAATGTACCTTGGCACCTC	52	124	124	>200	>200	1	1
91001210	pm1235	20	AGCCATCTGGTTATGTCTTA	CCACATCTCCACAGGGAGT	44	90	90	>200	>200	1	1
91001377	pm1701	20	TCCATGCTGTTAGAAAGCCAG	TTTATAGTGCACACAGAGT	54	142	142	>200	74	1	1
91001385	pm2101	21	GTGAGCTCAATGCTACACAG	TTTATAGTGCACACAGAGT	45	130	130	180	>200	1	2
91001427	pm0648	21	CTTCTGCTATAAAGTAGAG	ACAATGGTCTCACTAAATGA	39	58	58	145	>200	1	1
91000978	pm0912	22	GGTAGTAGTAAACATTAG	AGTGCACCCATCTCTCTGC	46	124	124	>200	>200	1	1
91001444	pm0911	22	GGTCTGTCTCTCCATCTGT	AGAAAGCCCAAGAGTAGTCC	40	65, 80	65	100	125	1	2
91001473	pm2231	22	TGAGCTGCACCTACCTGTGAGAG	AGCAGGTGAGTGGGTCTTCT	50	94	94	67	135	2	6
91001479	pm2228	22	TACAGCCCTCCACAGCTAAC	TTTATCTGCATCCACTACAA	46	65	65	190	>200	1	1



Fig. 9

g1-000999	pml759	X	CTGCCATAGTTACCTGGATT	TACCCACCACATATTAGCA	47	103	103	-	-	-	1	1
g1-001149	pml2180	X	GGAGGGGAGATATAGATTGT	AAAAATCCAGAGACATGA	46	70	70	135	150	-	1	1
g1-001161	pml6508	X	TTCATAGTGTGACCAAGTT	GGAGGATTGAGATACACAT	40	85	85	>200	>200	80	2	3
g1-001166	pml289	X	TAAATCCAGTGAATGTTCGTAA	GTAAGCTTATCTTCATCAGA	47	82	82	>200	80	-	1	1
g1-001166	pml289	X	ATCCTCTGAAATACATCTG	GGGAGAGACATCACATGAC	46	70	68	130	-	-	1	1
g1-001166	pml113	1,18	TATCCATGACATCTCTAT	AATACAACTTAACACAA	44	69	69	170	-	-	1	1
g1-001166	pml2272	1,2,3,5,8,12,14,17,X	GTCCAGTGGAGTGAAT	TTTATGTGTTCCTCAAGT	43	130	130	150	132	2	2	2
g1-001166	pml314	1,2,6,X	TATCAAGTGAATATGTCAC	TTATGTATACAAAGCACT	45	93	93	110	-	-	1	3
g1-001166	pml1461	1,3,4,5,8,16	TCCAAATGAAAGGTGTA	AGTIGACAGCCAGGTGAATG	43	96	96	100	100	-	1	3
g1-001166	pml561	2,20,21,22	GTCTGCAAGCCAGATTC	TTATATGGTGTACACTCG	43	110	110	170	150	-	1	1
g1-001166	pml2795	2,4,5,10,12,15,17,20,22,Y	GACCTGTGACATCTGGACT	TTATATGGTGTACACTCG	43	61	61	-	-	-	2	6
g1-001166	pml912	2,5,14,C	GCCTGTGATTTCCCACTC	ATCCCTTTCCTCCAGTTA	46	82	82	>200	82	-	1	1
g1-001166	pml1853	2,8,12	TCTGAGCAGATTCACAGCAG	CAGTCAAAACCAACCGGTAT	49	95	95	93	160	-	1	1
g1-001166	pml1778	2,9,13,17,X	TGCATTAAGGGAAGACCA	CCGTGTAGGTGATGAATG	49	78	80	>200	>200	-	1	2
g1-001166	pml885	20,X	GTCAATGTATGCAATTC	ACATTTATTTTTCACG	37	45	45	-	-	-	1	2
g1-001166	pml457	3,10,15	CATGTACTCAGAGGCACTC	GCACCTACAAATCCCAACT	50	133	133	>200	150	2	2	2
g1-001166	pml2651	3,4,M	CAGGACTGGAGCAGGAAG	GATTAACCCATTAGGAGC	50	101	101	101	88	3	3	3
g1-001166	pml2632	3,5	TTAGGAATATGGTTAGACAG	ATAGTATGGGTGACACATGA	43	80	80	>200	120	-	1	1
g1-001166	pml133	3,8	TGGATTCCTTACCTGTT	ACAGCCICAGGAGATGTTAC	47	93	93	95	>200	-	1	1
g1-001166	pml250	3,9,10,15	GCACACAGGCCAATCAGA	CCTTTAACACCAACAGCAG	50	96	96	>200	125	2	10	10
g1-001166	pml676	4,6	GGATTTCTATTCTGTCTAT	GTATTGTACGGCATTTAC	44	105	100	>200	>200	-	2	4
g1-001166	pml234	6,20	GCATTAAACGGAACATA	CTGTCCATGTGCAATAAAC	44	110	110	105	107	-	1	1
g1-001166	pml608	7,18	AGATGCTATCATTAGGATA	TTTTCAGATACAGAGGAGT	43	81	81	102	-	-	1	1
g1-001166	pml253	9,11	CCAGACTACAGGCTATGCG	CCCTTACCCAGCACTCTT	55	75,130	75	>200	>200	-	1	1
g1-001166	pml115	9,M	ACCAATGCTACGCTCTTAAATA	CCCAATAAGTGAAGGTAGTTC	48	125,155	127	125	>200	-	1	1
g1-001166	pml478	10,15,22	AGGAATGTTTACTGGATT	TTATCTGACTTGGAGGAAT	42	107	107	-	-	-	1	1
g1-001166	pml2420	10,15,22	ACTACCCCTGAAATATAGTT	TTCAITTTATTTGATTGTA	46	100	100	170	-	-	1	1
g1-001166	pml2103	11,M	ATACCACTCCGCTGTCAGG	GAGAGGCTCTACTGGTCTT	50	72	74	72	>200	3	20	20
g1-001166	pml2642	12,19	GCACCAAGAGCAGTTCAG	TTGGAAATGAGAAATAACT	46	83	83	81	-	-	1	7
g1-001166	pml2773	12,M	GATCTGATTTCTGCGTTTAT	TACATACAAAGATGCAACAGT	44	80	80	79	68	-	1	1
g1-001166	pml2725	13,16	ATCTGTGTGCTGCTTCC	GTCTCTCTCTGATGGCTGA	46	62	60	135	180	-	1	1
g1-001166	pml2780	14,16	AACCTGTTTACCCGATCTT	AGGTATTTGTCACACAGAA	48	87	87	>200	>200	-	1	1
g1-001166	pml683	17,20,C	TGTTGGTTCACCATGAGAC	AGAACACACATCAAGATGC	46	90	90	>200	90	-	1	1
g1-001166	pml1748	17,22,Y	GAATGTCATCCAAAGAGTAG	CTAGTTATCTGCGCTG	44	81	81	>200	200	-	1	1
g1-001166	pml964	17,C	TTTATCCAGCAGCAGCAAC	TCCTCTCTCTCTCTCTCT	49	120	120	>200	170	4	11	11
g1-001166	pml2217	17,C	ACTAAAGTAGCTTTGACG	TGCTCTCTCTCTCTCTCT	43	95	95	>200	95	-	1	1
g1-001166	pml1213	18,C	CCCGAGTTAAGATATGTT	AGTACGATGGAGGATGTA	44	92	92	-	92	-	1	1
g1-001166	pml1118	19,20	TGAGAGTAGTTTCCAGAG	CGTAGGATCTCTCTCTCT	46	75	72	160	65	-	1	1
g1-001166	pml2824	19,22	ATCCCTCTCTCTCTCTCT	GCTGTTTAACTCACTCTCAC	46	110	110	130	170	2	2	2
g1-001166	pml887	19,22	CCCTGATCTGTTGACTT	AACCTCTGGCAACAAATCAT	48	91	89	160	86	-	1	1



Fig. 10

g1001057	pm2049	C	AGGACACAAACAGCAGCTAT	TTTCTGATTATGACATGAC	45	75	75	101	75	1	1
g1001173	pm1753	M	ATCTCTTTGAGCCATCTCG	GTTAAGTGTGATGCCATT	42	64,100	64	64	>200	1	1
g1001056	pm2236	N	GTAGAGCTGCATTGACTACC	ACAGACAGGAATAATCAT	42	108,96	110	110	112	1	1
g1001166	pm506	N	GTCCACAGCTCCAGCCTAAC	GCCACATATTAAGATCCATC	46	74	74	74	>200	1	1
g1001151	pm2354	N	TGTTTGTGGAGCTCTGCCT	TTTAAAGTCAATAATACATGTT	44	110	110	110	106	1	1
g1000279	pm2492	M,C	GCTAGAAAGAGGGCACTCA	CTTAACTCGATAGCCAGGTC	46	75	75	75	75	1	1
g1000253	pm2786	M,C	CACAAACAGCAAACTTCAG	ATGGTTATTTATCAGATTG	41	83	83	82	83	2	3
g1000285	pm1704	M,C	TCCACCAGAGAGACACACT	AATCTATAGGGAATAGGTTTC	40	75,130	75	75	75	1	23
g1000302	pm2318	M,C	TCGAAAGAGCAAAATCACCC	GAACAGGGTTAGTCCATTCG	48	50	50	50	58	1	1
g1000541	pm1689	M,C	CATGAGCTACGGAAACAGG	AGGAGTCCGTGGGTCTTGAG	51	81	84	84	84	4	18
g1000675	pm1442	M,C	AAGCATCTTGAGAGGACAC	GGAGGACTCGCTTGGCTCTTA	49	110,200	110	110	110	1	9
g1000732	pm1452	M,C	GCAGCAGTACCTTTACACC	TGGTTCAATTCAATTCTCTTC	51	102	105	102	102	3	13
g1000985	pm286	M,C	GAAGCTCTTGAGGAAAGCT	CAGACCCCATCTTTATACC	47	79	79	79	79	3	4
g1001016	pm2703	M,C	ACGATATTATAGTATGTTG	TCAAACTTTAATATATGCT	40	93	93	91	92	1	1
g1001053	pm1144	M,C	AGTGAAGTGTGGTCAGAGA	CCATTCCTGTCATCCAGTT	52	135	140	135	135	1	1
g1001127	pm2200	M,C	ACTGGTATGGAAAGTTTACA	CCACAGAGTGAGCCGCTCT	47	55	55	55	55	1	1
g1001167	pm1626	M,C	TAGTCAGAGATTCACTAAGT	CTTCCCTTGGCTCTTCTGT	49	100	100	100	100	1	1
g1001216	pm2109	M,C	AAGAGAGCTTGCATCCTTFA	ACATGTATTTGATAGTCTT	42	110	110	110	110	1	2
g1001253	pm1240	M,C	AACTGGTTCATCAAGACCTG	AGTGAAATAACTTCCACTCC	48	120	120	120	120	1	1
g1001281	pm1131	M,C	ACTTAAACCCCAACAGCAT	ACACACAGCTCAATAGAA	47	97	97	97	97	1	1
g1001375	pm0952	M,C	AAGAGGAGTTTCCCTCTCA	ATGATGCGAGAGCGCAAGGA	51	89	89	89	150	1	1
g1001356	pm2216	M,C	ATCTGCATGACCTATATCT	CGTCTCTTTTATTTGACAT	45	108	108	108	108	1	1
g1001411	pm0958	M,C	ATGGGTTTATCAGGGGTTTC	GAGACAAAGCACTCTCTTA	47	80	77	80	80	1	1
g1001460	pm2626	M,C	ACATTGATGGGATGAGGT	GGACATTTCTAGCCCAAGC	51	75,55	75	75	75	1	2
g1001482	pm1210	M,C	TTGTGACATTCCTTTTAGAA	CAGTCCCTCTGACTGAGACA	40	85	85	85	85	1	2
g1001450	pm0109	M,C	GCCACAGACATCATCCT	TCTTAGTAGGTGCTCTGGTG	51	98	98	98	98	1	1
g1003108	pm2042	No product	CAACCAAGTAGCGTGAAGCT	GAATATCCCTTGTCTCTA	45	87	87	87	87	1	1
g1000050	pm0304	No product	CTTTGGGATATTTCTTCAT	CCCTCGGCTACTTTCTATG	43	60	60	62	62	1	2
g1000683	pm0808	No product	AGCCAGCCTCTTGTATGTG	CTGGATTGATTTTCATAG	44	87	87	87	112	1	1
g1001254	pm1673	No product	TGTGGTATGAAATATCTGA	TTATGAAATGAGACAACACT	43	80	80	163	>200	1	1
g1001355	pm2908	No product	CAGTAGTGTGCTTGAAATG	TTTATGGAATGTGGTTGT	41	63	63	63	150	3	3
g1001373	pm0361	No product	TACAGCCGCTCTTAAAGTC	TTTGAGCATCAAGGAATCT	48	82	82	82	>200	1	1
g1001556	pm0849	No product	TACATCTTCAGACTCATCG	TTTTCAAAACCTTATCTT	40	86	86	86	>200	1	1
g1001574	pm1284	No product	ATCAGAGCTCAGTCTGTAG	ATTTCGCTCTTGCATGGTC	44	57	57	67	67	2	2
g1001672	pm1606	No product	GATCTTGAGCCTTAAGTGA	TTTGCAGTTCAGCTTATTC	45	54	54	54	54	1	1
g1001640	pm0852	No product	GATCTGTCTCTTTCACA	TTTATACAAAGCACCATAC	30	45	45	45	45	1	1





Fig. 11

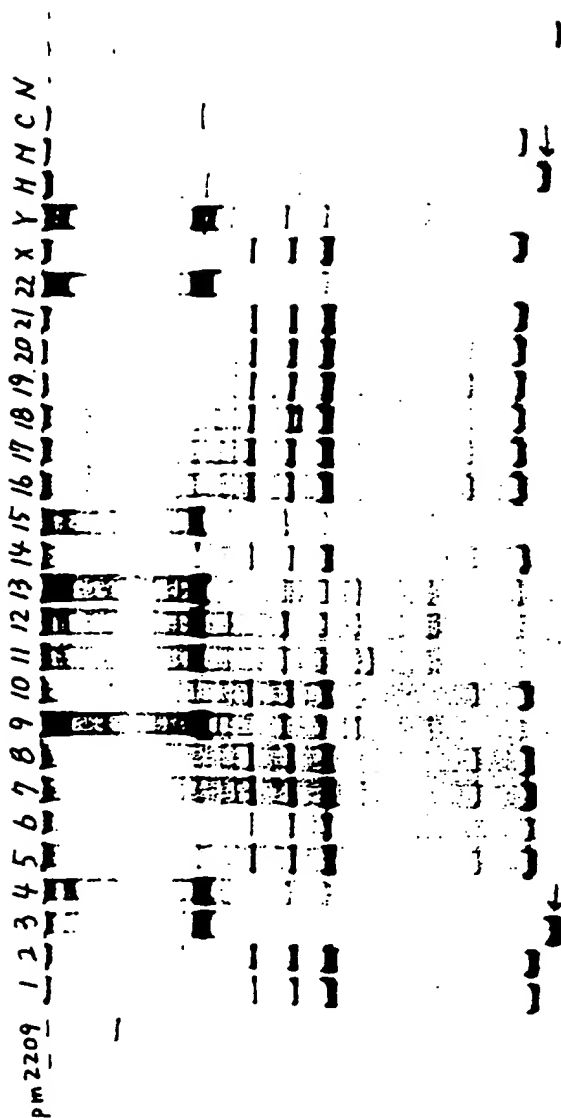




Fig. 12

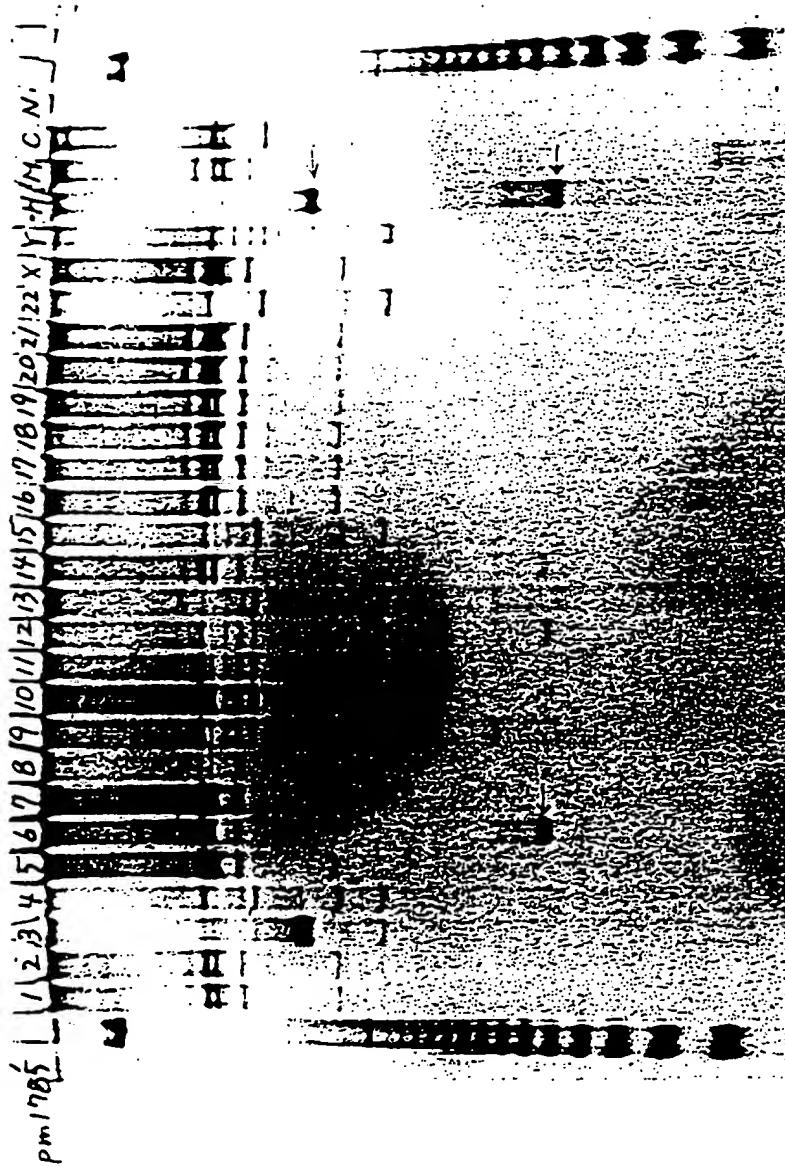




Fig. 13

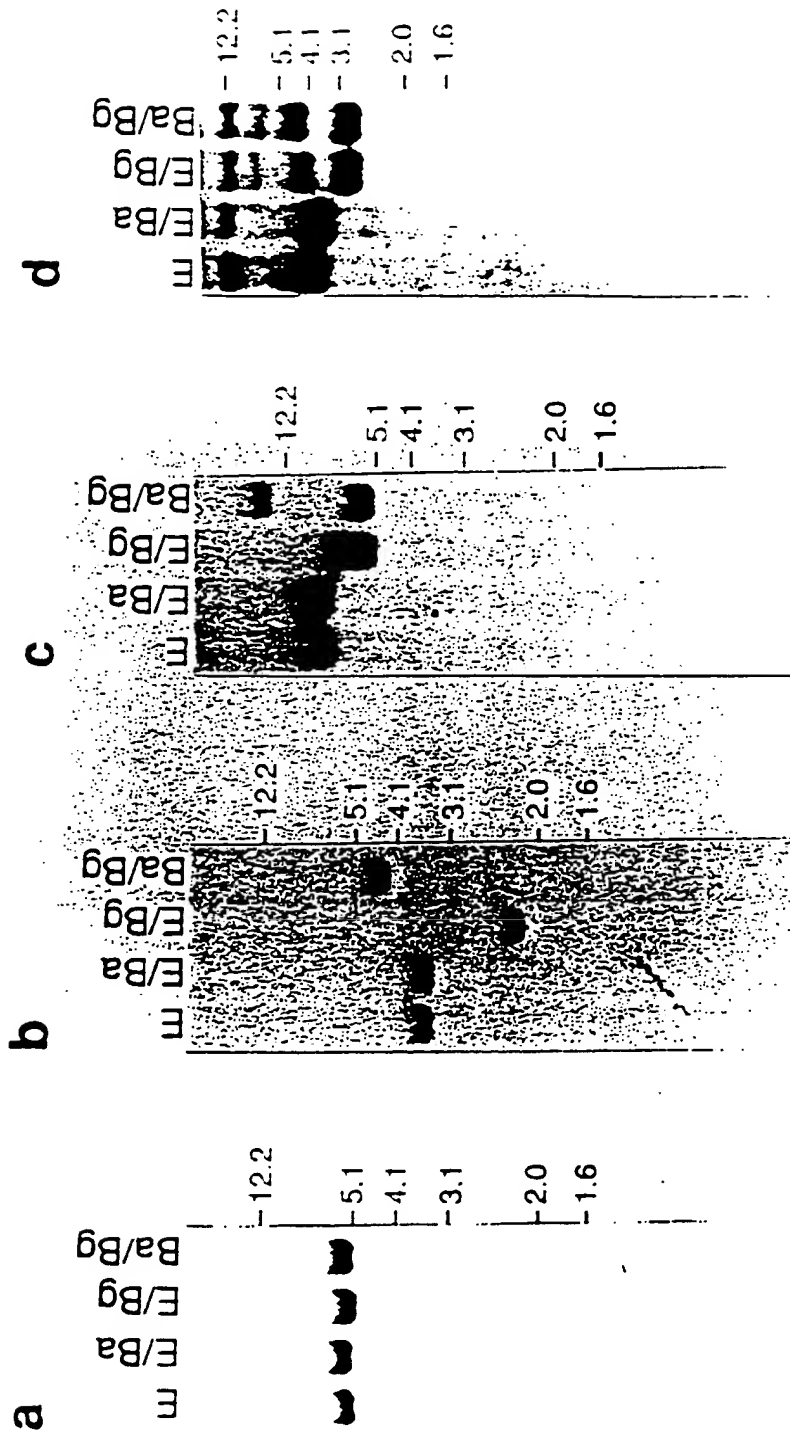




Fig. 14

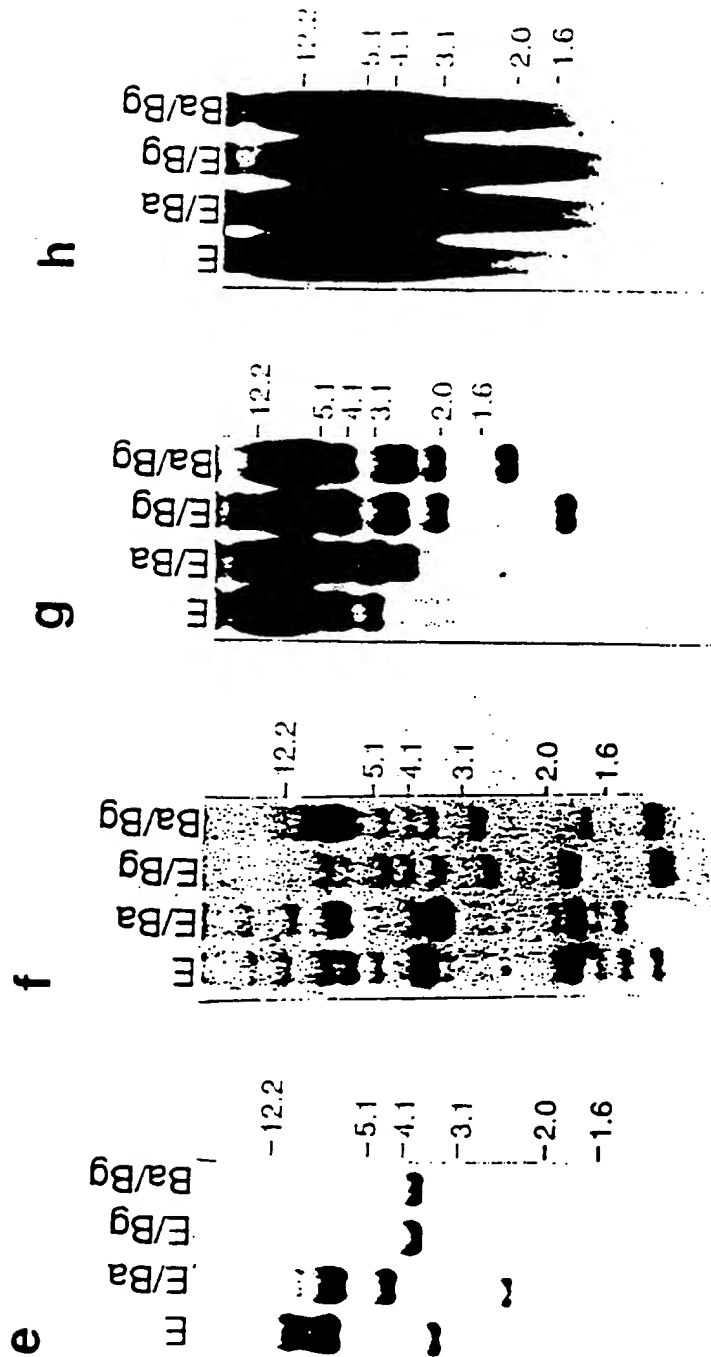






Fig. 15

## Hybrid cells used for Southern hybridization

Hybrid cell	Human chromosome No.	Parent cell	Intact chromosome (%)	Translocated chromosome (%)
A9(neo-1)-4	1	A9	100 (0)	0
A9(neo-2)-1	2	A9	93 (8)	0
GM10253	3	CHO	100 (0)	0
GM10115	4	CHO	100 (0)	0
A9(neo-5)-4	5	A9	40 (0)	90
A9(neo-6)-3	6	A9	100 (60)	0
A9(neo-7)-2	7	A9	100 (89)	0
A9(neo-8)-1	8	A9	91 (82)	0
GM10611	9	CHO	79 (5)	11
A9(neo-10)-3	10	A9	94 (6)	75
A9(neo-11)-1	11	A9	24 (0)	76
GM10927A *	11	CHO	96 (21)	4
A9(neo-12)-4	12	A9	0 (0)	100
GM10868 *	12	CHO	82 (6)	0
GM10898	13	CHO	82 (0)	10
GM10479	14	3T6	76 (29)	0
A9(neo-15)-2	15	A9	9 (0)	78
GM11418 *	15	CHO	62 (0)	100
GM10567	16	A9	69 (0)	0
GM10498	17	LTMK	80 (10)	0
A9(neo-18)-5	18	A9	100 (66)	0
A9(neo-19)-1	19	A9	92 (23)	8
A9(neo-20)-3	20	A9	81 (5)	17
GM08854	21	A9	81 (24)	0
GM10027	22	CHO	93 (0)	100
GM10324	X	A9	81 (10)	0
GM06317	Y	CHW1103	91 (0)	9



Fig. 16

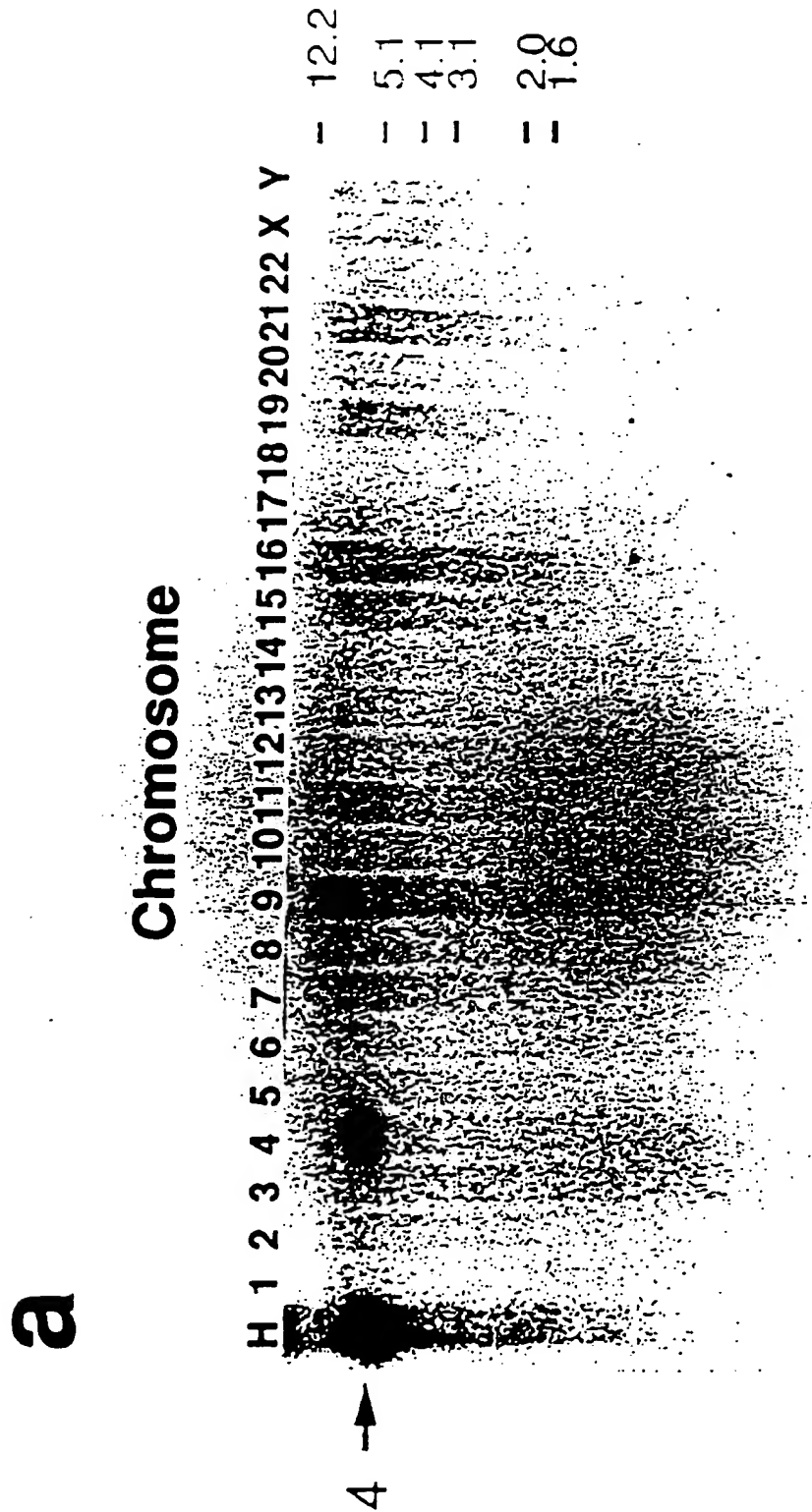




Fig. 17

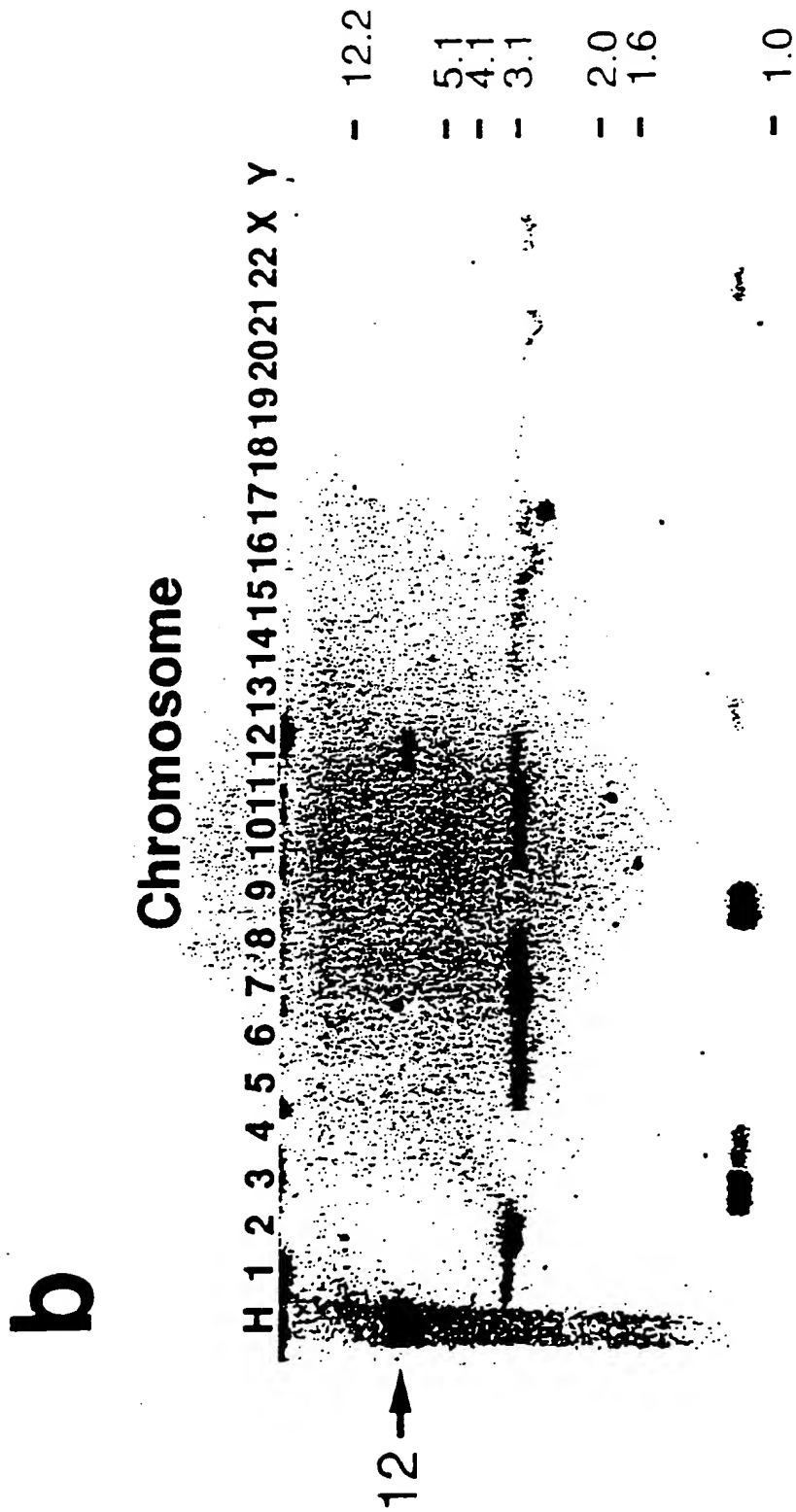




Fig. 18

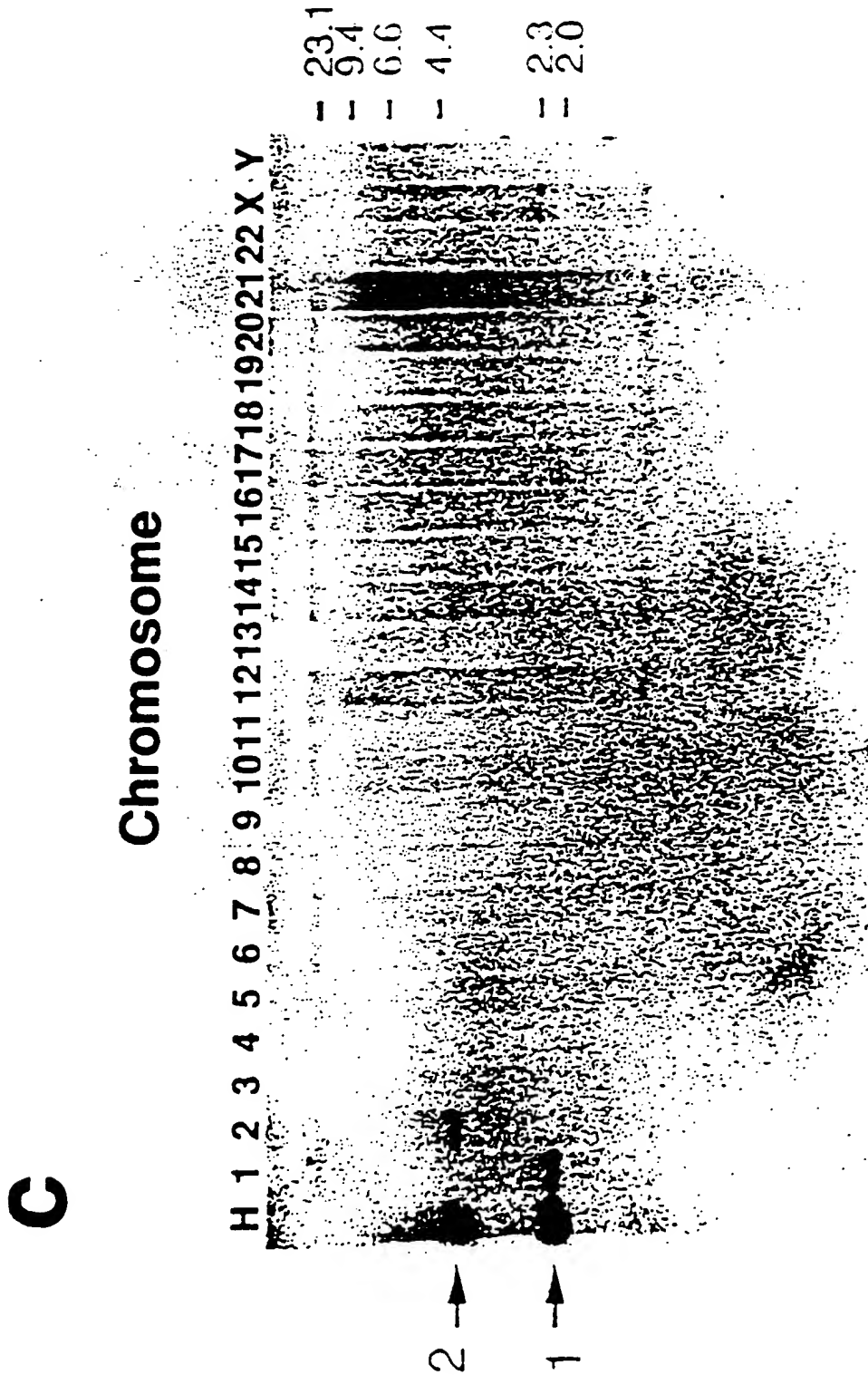






Fig. 19

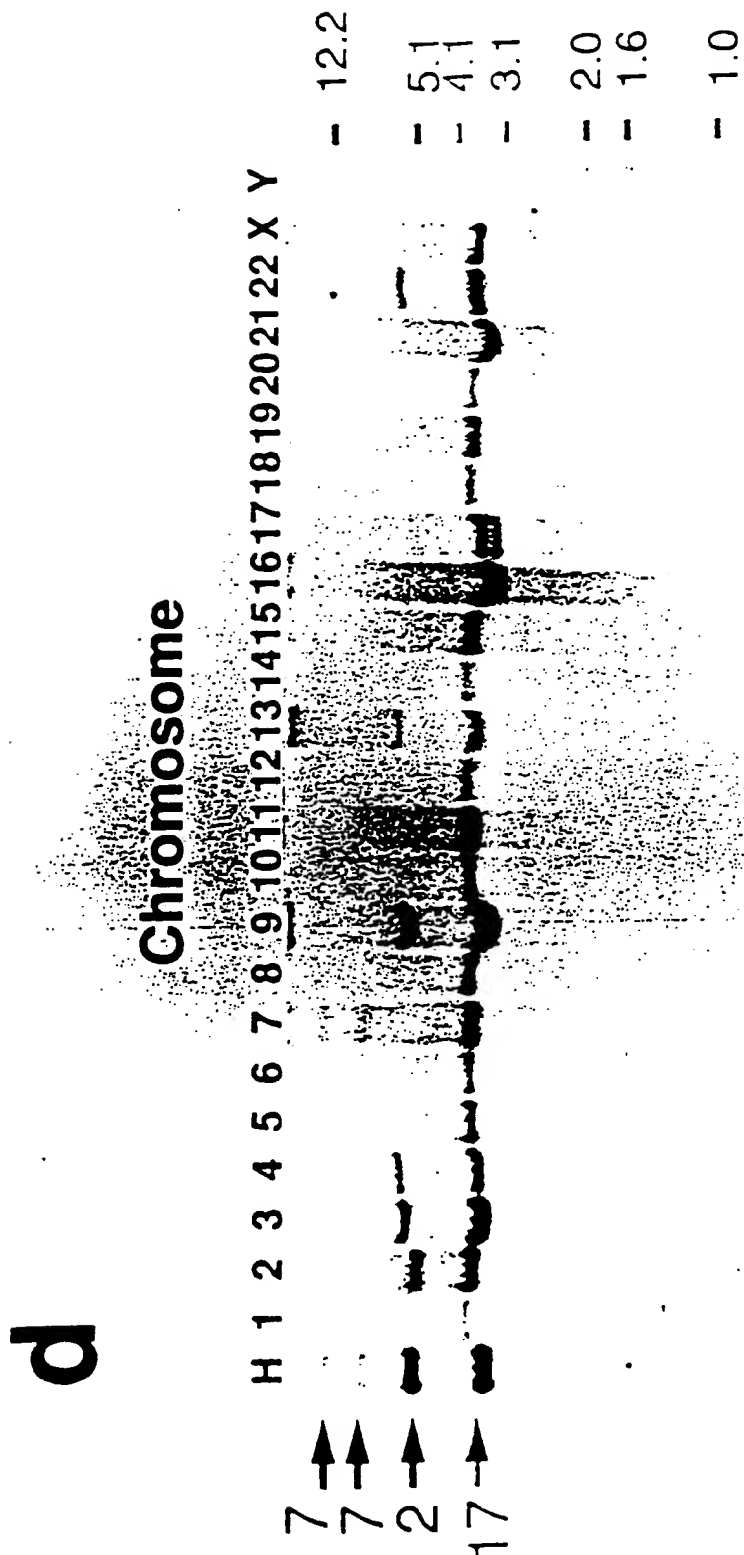




Fig. 20

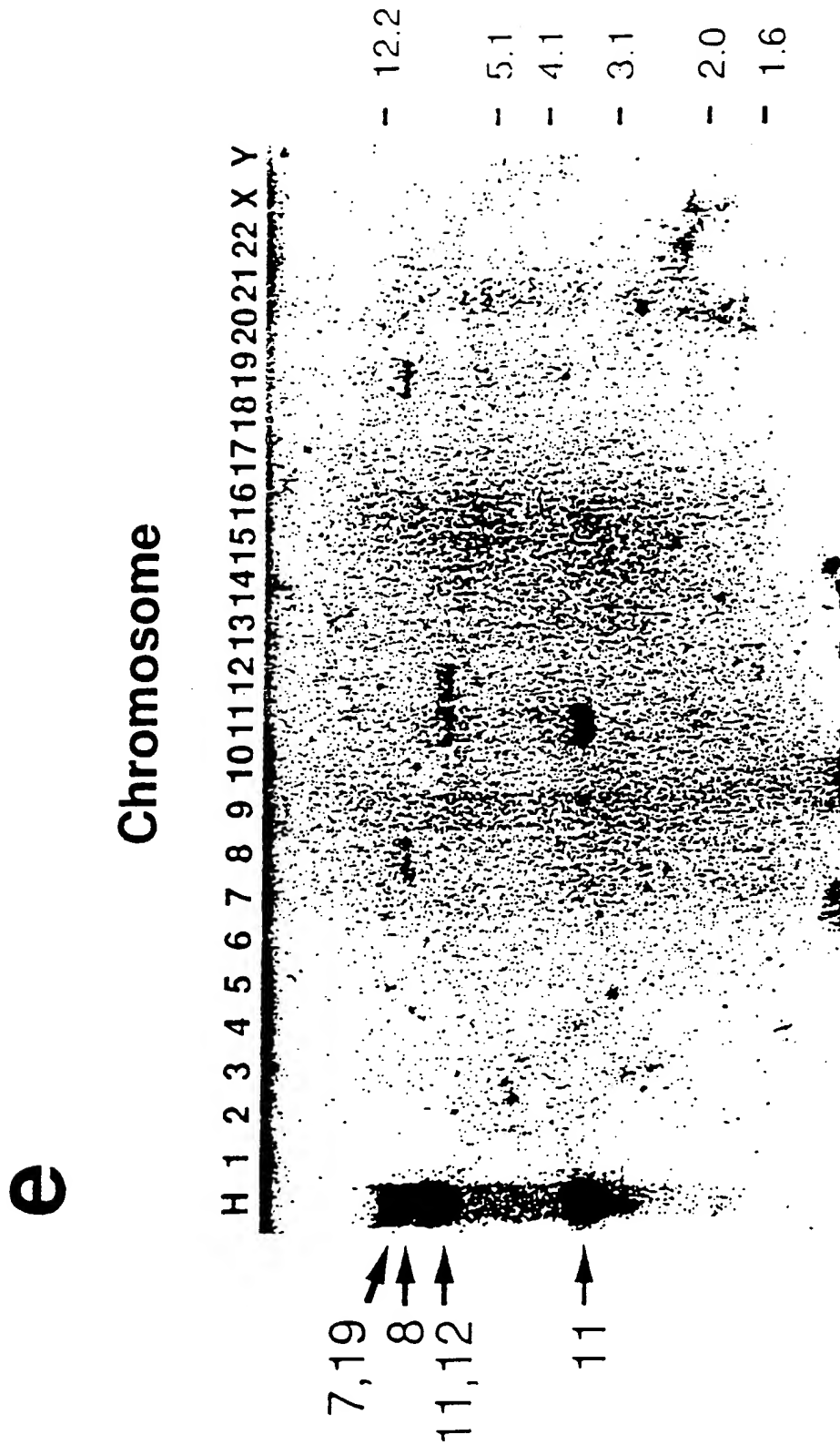




Fig. 21

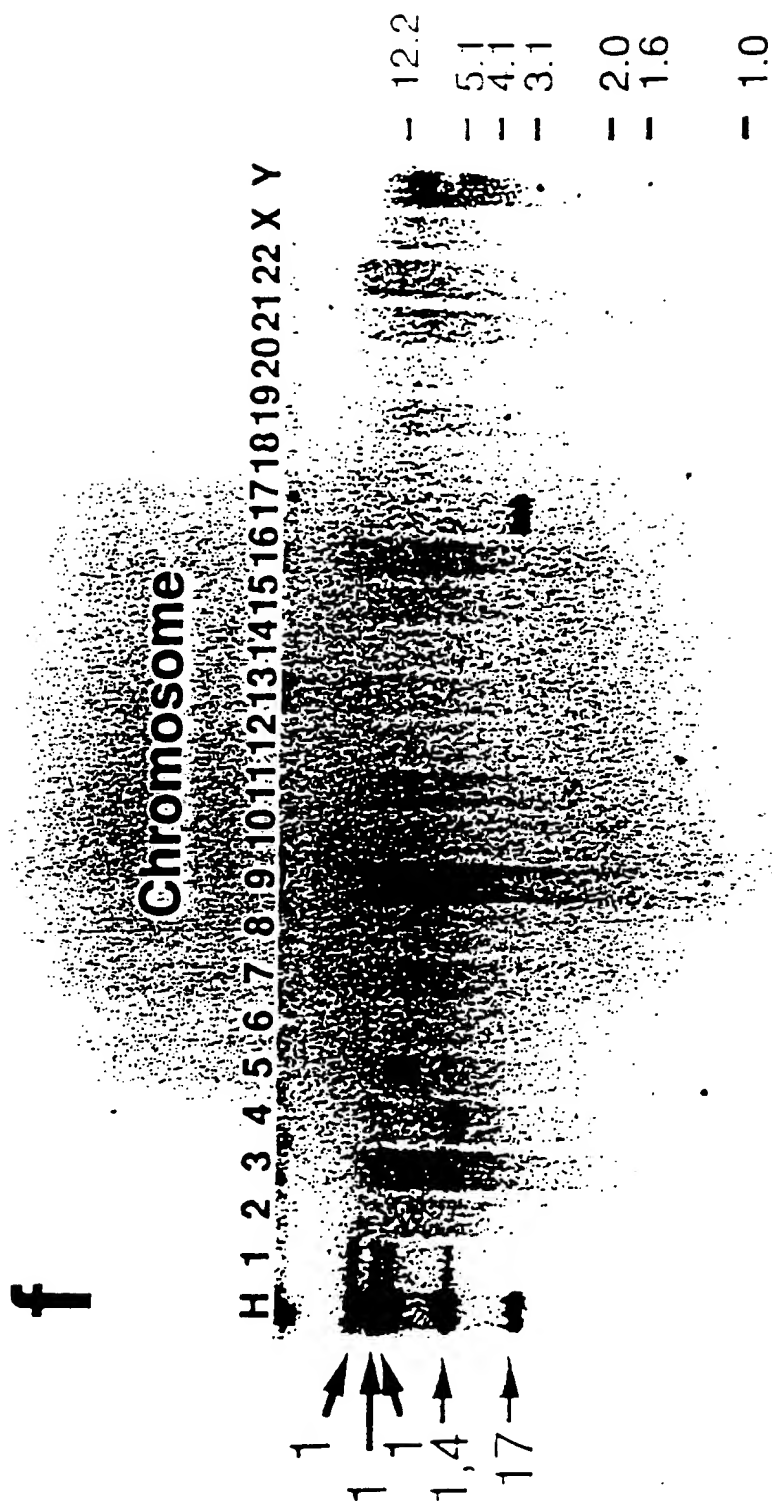




Fig. 22

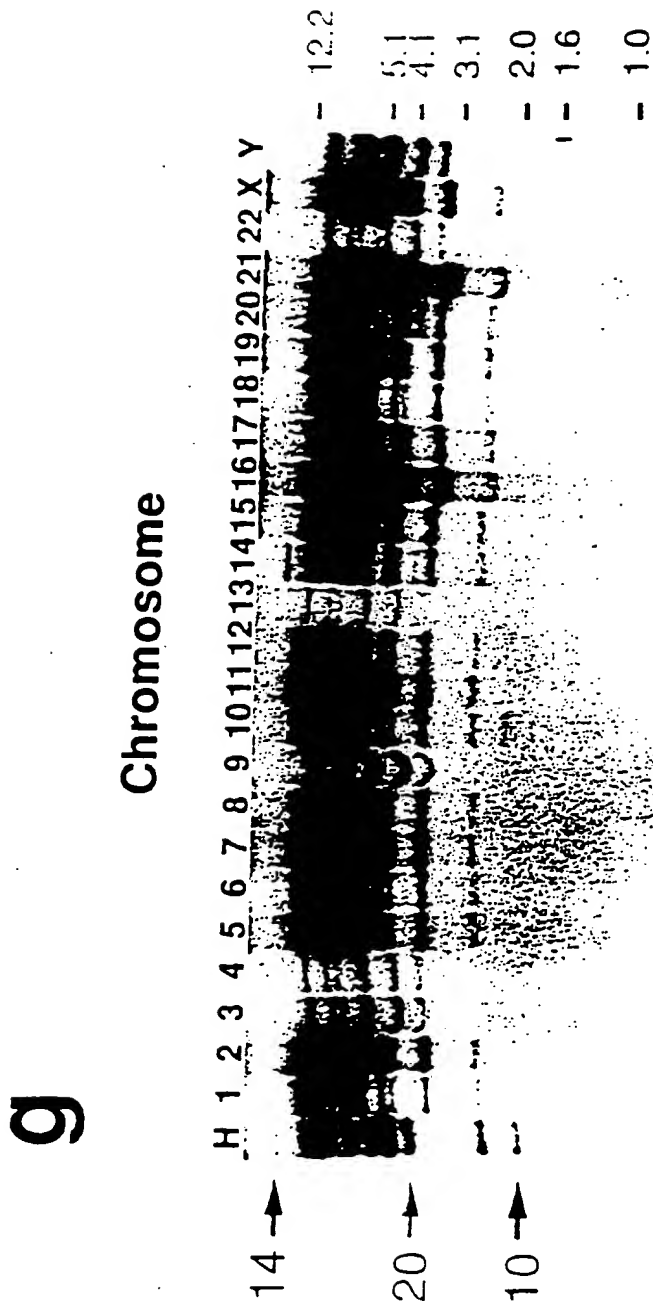






Fig. 23

Chromosomal mapping of each GS by Southern blot technique

Numbers of bands detected with human whole chromosomes					Chromosomes assigned		Background	
Clone	Sequence length	≡	≡/≡	≡/≡	≡/≡	Mouse	Chinese hamster	
Single band group:								
c12a11	GS000073	432	1	1	1	9	0	0
c12e06	GS000062	540	1	1	1	5.15	0	0
c12g01	GS000290	212	1	1	1	2	1	1
c13e05	GS000117	359	1	1	1	11-	0	0
c13e07	GS000129	355	1	1	1	2	0	0
c13f10	GS000208	257	1	1	1	14	0	0
c13h01	GS000279	133	1	1	1	12-	0	0
c13h02	GS000222	167	1	1	1	6	0	0
d0g02	GS000095	397	1	1	1	3	0	0
d0h07	GS000154	313	1	1	1	11	1	1
d1b10	GS000348	153	1	1	1	20	0	0
hm01a12	GS000223	246	1	1	1	47	0	0
hm01c09	GS000423	157	0	1	1	1	0	0
hm01e12	junk	394	1	1	1	17	0	0
hm01f05	GS000066	454	1	1	1	19.22	0	0
hm01f10	GS000299	173	0	1	1	10	0	0
hm01g09	GS000053	477	1	1	1	6	0	0
hm01h07	GS000115	363	1	1	1	12	0	0
hm02a02	GS000130	344	1	1	1	4	0	0
hm02a04	GS000329	164	1	1	0	10	0	0
hm02e01	GS000293	271	1	1	1	15	0	0
hm02e01	GS000015	590	1	1	1	20	0	0
hm02e02	GS000342	156	0	1	1	14	0	0
hm02e05	GS000401	225	1	1	0	n.d.	0	0
hm02g02	GS000191	273	1	1	1	17	0	0
hm05a05	GS000251	219	1	1	1	6	2	0
hm05a10	junk	392	1	1	1	1	1	1
hm05e10	GS000009	606	1	1	1	1	0	0
kmd01	junk	169	1	1	0	n.d.	0	0
s105	GS000001	703	1	1	1	5	0	0
s110	GS000057	471	1	1	1	3	0	0
s11d11	GS000307	#175	0	0	1	7	0	0
s11h01	GS000259	204	1	1	1	3	0	0
s147	GS000060	461	1	1	0	2	0	0
s14e06	junk	639	1	1	1	1	0	0
s14g02	GS000152	322	1	1	1	4	0	0
s14h12	GS000271	193	1	1	1	4	1	1
s150	GS000143	330	1	1	1	17	0	0
s156	GS000002	306	1	1	1	2	1	1
s15b11	GS000250	221	1	1	1	14	0	0
s179	GS000275	196	1	1	1	n.d.	0	0
s246	GS000224	241	1	1	1	7	0	0
s247	GS000347	153	1	1	1	1	0	0
s270	junk	135	1	1	1	19	0	0



Fig. 24

Numbers of bands detected with human whole chromosomes		Chromosomes assigned						Background	
Clone	Sequence length	≡	≡/3:	≡/3:	3≡/3:			Mouse	Chinese hamster
s306	GS000255	205	1	1	0	1	X	0	0
s309	GS000171	305	1	1	0	1	1	0	0
s342	GS000323	165	1	1	1	1	4	3	2
s331	GS000295	207	1	1	0	1	6,15	1	1
s334	GS000165	312	1	1	1	1	1	0	0
s337	GS000275	195	1	1	1	1	17	0	0
s339	GS000295	130	1	1	1	1	n.d.	0	1
s443	GS000330	251	1	1	1	1	n.d.	0	0
s470	junk	251	1	1	1	1	17	0	0
s474	GS000192	273	1	1	1	1	5	0	0
s503	junk	312	1	1	1	1	12	0	0
s507	junk	600	1	1	1	1	1	2	1
s517	GS000334	161	1	1	1	1	14	1	1
s632	junk	587	1	1	1	1	2	0	0
s633	GS000166	311	1	1	1	1	22	2	1
s650	GS000041	644	1	1	1	1	12	1	1
tw1-04	GS000025	537	1	1	1	1	3,7	0	0
tw1-19	GS000213	255	1	1	1	1	17	0	0
tw1-32	junk	250	1	1	1	1	5	0	0
tw1-37	GS000237	235	1	1	1	1	22	0	0
tw1-42	junk	391	1	1	1	1	3	1	1
tw1-43	GS000093	178	1	1	1	1	14	0	0
tw1-96	GS000133	339	1	1	1	1	11	0	0
Two band group:									
e12f12	GS000195	277	1	2	2	2	1,	1	1
e13d02	GS000042	503	2	2	1	1	2,	0	0
hm01a06	GS000129	344	2	2	2	2	11,13	3	3
hm01a07	GS000207	259	2	2	2	2	7,	0	0
hm01d05	GS000232	243	2	2	2	1	2,	0	0
hm01e01	GS000131	292	2	2	2	2	1,2	0	0
hm02a03	GS000435	302	2	2	2	2	3,	1	1
hm02e04	GS000221	253	2	2	2	2	3,	0	0
hm02e05	GS000146	332	2	2	2	2	17,19,22	0	0
hm05f07	GS000043	503	1	1	2	1	3,	0	0
s11d06	GS000268	205	2	2	2	2	11,12	0	0
s11g12	GS000337	255	2	2	2	2	6,	0	0
s124	GS000083	404	2	2	2	2	9,	1	1
s144	GS000132	342	1	2	2	2	1,7	0	0
s14f03	GS000239	243	1	2	2	2	2,	3	2
s15e02	junk	439	2	2	1	2	6,	0	0
s16b09	junk	420	1	1	1	2	10,14	0	0
s17e09	GS000248	223	2	2	2	2	14,	0	0
s231	junk	234	2	2	2	2	11,	0	0
s254	GS000124	353	2	2	2	2	1,	3	1
s255	GS000235	239	2	2	2	2	11,	0	0
s272	junk	193	2	2	2	2	10,16	1	1



Fig. 25

Numbers of bands detected with human whole chromosomes				Chromosomes assigned				Background	
Clone	Sequence length	E	E/B <sub>1</sub>	E/B <sub>2</sub>	B <sub>1</sub> /B <sub>2</sub>			Mouse	Chinese hamster
s311	GS000092	333	1	1	2	2	16,	1	1
s313	junk	132	2	2	1	0	20,	0	0
s317	GS000100	139	0	0	1	2	14,14	1	1
s336	GS000134	337	2	2	2	2	12,14	0	0
s333	GS000139	233	2	2	2	1	22,X	0	0
s339	GS000233	137	2	1	1	2	17,	0	0
s394	GS000063	449	2	1	2	2	13,14	0	0
s396	junk	277	2	2	2	2	17,	0	1
s455	junk	452	1	2	2	1	4,	0	0
s456	GS000236	132	2	2	2	2	8,10	1	2
s465	GS000201	274	1	1	2	2	6,15	0	0
s635	junk	250	1	1	1	2	9,13	0	0
s639	GS000297	205	1	2	2	2	2,X	0	0
s656	GS000025	0590	2	2	0	2	6,11	0	0
tw1-33	junk	352	2	2	2	2	1,	0	0
tw1-39	GS000153	0321	2	2	2	2	17,	0	0
tw1-70	GS000061	441	1	1	2	1	11,	0	0
tw1-80	junk	453	2	2	1	2	9,17	2	2
tw1-87	GS000158	316	2	2	2	2	7,	0	0
Three band group									
d0h06	GS000030	417	3	3	3	1	1,	0	0
hm05b07	junk	336	2	3	3	3	5,	0	0
hm05g02	GS000209	267	2	2	2	1	3,17,19	1	1
s129	GS000107	373	3	3	3	3	n.d.	1	1
s173	GS000357	146	1	2	2	3	2,	0	0
s17s10	GS000294	181	3	3	3	3	2,13,22	1	1
s308	GS000412	638	2	2	2	3	X,X	1	1
s401	GS000224	249	2	3	3	3	6,5,	0	0
s654	GS000045	491	3	3	3	3	1,22,	0	0
tw1-82	GS000208	267	3	3	3	3	13,	4	0
Four band group									
c12g07	GS000154	320	4	4	2	3	5, 14,	0	0
c13s08	GS000053	308	3	3	4	4	2,7,7,17	1	2
c13e04	GS000108	0376	4	3	3	3	n.d.	0	2
c13e09	GS000302	195	4	2	4	4	2,17,	7	2
s136	GS000160	315	4	4	4	4	4,X	2	1
s163	GS000004	0618	4	4	4	2	4,4,8,20	3	1
s479	GS000130	293	4	4	2	2	7,8,11,11,12,19	0	0
Group with 5 or more bands									
c12r08	GS000253	217	5	5	5	2	2,7,9,14,	2	0
he01	junk	374	12	12	13	18	1,2,6,	22	20
hd10	junk	361	4	4	4	8	n.d.	12	6
he10	junk	173	6	2	3	3	6,3,9,19,21,	3	3
hm01c05	GS000205	176	9	7	5	5	X	9	8
hm01r04	GS000246	215	8	10	5	5	n.d.	12	12
hm01g02	junk	411	9	6	6	4	10,14,20,	14	6



Fig. 26

Numbers of bands detected with human whole chromosomes						Chromosomes assigned	Background		
Clone	Sequence length	3	3/3 <sub>1</sub>	3/3 <sub>2</sub>	3 <sub>1</sub> /3 <sub>2</sub>		Mouse	Chinese hamster	
hm02f09	GS000273	442	3	7	7	5	3,3,6,11,13,14,15,16	0	0
hm03a02	GS000096	173	5	6	4	6	2,3,17	3	3
hm03a04	GS000236	#239	6	6	6	7	n.d.	8	5
kmb01	junk	350	3	5	5	5	13	14	7
s11f06	GS000315	170	6	6	6	4	1,2,2,3,4,6,13,15	0	3
s14f01	GS000407	242	12	11	10	9	1,5,9,13	6	3
s173	GS000094	397	5	4	5	3	1,1,1,1,4,17	0	0
s255	GS000323	167	10	12	11	14	13	9	5
s341	junk	494	9	9	3	6	n.d.	15	3
s406	GS000113	364	6	7	5	4	2,7,3,13,20,20	4	1
tw1-46	junk	593	9	10	10	10	1,1,2,2,5,11,X	3	5
tw1-63	junk	203	3	10	10	12	3,4	17	11
Bands no detected:									
e13g02	GS000340	157	0	0	0	0	-	-	-
hm01e10	junk	232	0	0	0	0	-	-	-
hm02d11	GS000274	196	0	0	0	0	-	-	-
s323	GS000273	194	0	0	0	0	-	-	-
s359	GS000199	279	0	0	0	0	-	-	-
s511	junk	233	0	0	0	0	-	-	-
s645	GS000012	#734	0	0	0	0	-	-	-
s647	GS000193	360	0	0	0	0	-	-	-
s651	junk	540	0	0	0	0	-	-	-





# INTERNATIONAL SEARCH REPORT

International application No.

PCT/JP94/01916

<b>A. CLASSIFICATION OF SUBJECT MATTER</b> Int. Cl <sup>6</sup> C12N15/11, C12Q1/68//G01N33/566 According to International Patent Classification (IPC) or to both national classification and IPC		
<b>B. FIELDS SEARCHED</b> Minimum documentation searched (classification system followed by classification symbols) Int. Cl <sup>6</sup> C12N15/11, C12Q1/68//G01N33/566 Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched Electronic data base consulted during the international search (name of data base and, where practicable, search terms used) BIOSIS PREVIEWS, CAS ONLINE		
<b>C. DOCUMENTS CONSIDERED TO BE RELEVANT</b>		
Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	Nucleic Acids. Res., Vol. 15, 1987, Ou, J. H. "Cloning and characterization of a human ribosomal protein gene with enhanced expression in fetal and neoplastic cells" p. 8919-8934	1-6 (164)
X	Differentiations, Vol. 33, 1986, Oshima, R. G. et al. "Comparison of mouse and human keratin 18:A component of intermediate filaments expressed prior to implantation" p. 61-68	1-6 (226)
X	J. Biol. Chem., Vol. 265, 1990, Wilkin, D. J. et al. "Isolation and sequence of the human farnesyl pyrophosphate synthetase cDNA:coordinate regulation of the mRNAs for farnesyl pyrophosphate synthetase, 3-hydroxy-3-methylglutaryl coenzyme A reductase, and 3-hydroxy-3-methylglutaryl coenzyme A synthetase" p. 4607-4614	1-6 (255)
<input checked="" type="checkbox"/> Further documents are listed in the continuation of Box C. <input type="checkbox"/> See patent family annex.		
* Special categories of cited documents: "A" document defining the general state of the art which is not considered to be of particular relevance "E" earlier document but published on or after the international filing date "L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified) "O" document referring to an oral disclosure, use, exhibition or other means "P" document published prior to the international filing date but later than the priority date claimed "T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention "X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone "Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art "&" document member of the same patent family		
Date of the actual completion of the international search February 6, 1995 (06. 02. 95)		Date of mailing of the international search report March 7, 1995 (07. 03. 95)
Name and mailing address of the ISA/ Japanese Patent Office Facsimile No.		Authorized officer Telephone No.



## INTERNATIONAL SEARCH REPORT

International application No.

PCT/JP94/01916

## C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	J. Biol. Chem., Vol. 266, 1991, Batra, S. K. et al. "Molecular cloning and sequence analysis of the human ribosomal protein S16" p. 6830-6833	1-6 (275)
X	Proc. Natl. Acad. Sci. U.S.A., Vol. 87, 1990, Ben-Ishai, R. et al. "A human cellular-sequence implicated in trk oncogene activation is DNA damage inducible" p. 6039-6043	1-6 (313)
X	J. Biol. Chem., Vol. 263, 1988, Fischer, R. et al. "Multiple divergent mRNAs code for a single human calmodulin" p. 17055-17062	1-6 (386)
X	J. Cell Biol., Vol. 108, 1989, Barnett, T. R. et al. "Carcinoembryonic antigens: Alternative splicing accounts for the multiple mRNAs that code for novel members of the carcinoembryonic antigen family" p. 267-276	1-6 (446)
X	J. Biol. Chem., Vol. 265, 1990, Natsumeda, Y. et al. "Two distinct cDNAs for human IMP dehydrogenase" p. 5292-5295	1-6 (454)
X	Genes Dev., Vol. 7, 1993, Patton, J. G. et al. "Cloning and characterization of PSF a novel pre-mRNA splicing factor" p. 393-406	1-6 (706)
X	Nucleic Acids Res., Vol. 16, 1988, Stanford, D. R. et al. "The complete primary structure of the human snRNP E protein" p. 10593-10605	1-6 (711)
X	Proc. Natl. Acad. Sci. U.S.A., Vol. 84, 1987, Inoue, C. et al. "Evolutionary conservation of the insulinoma gene rig and its possible function" p. 6659-6662	1-6 (723)
X	J. Immunol., Vol. 144, 1990, Jongstra-Bilen, J. et al. "Human and mouse LSP1 genes code for highly conserved phosphoproteins" p. 1104-1110	1-6 (741)
X	Biochem. J., Vol. 248, 1987, Sakai, I. et al. "The cDNA and protein sequences of human lactate dehydrogenase-B" p. 933-936	1-6 (772)



## INTERNATIONAL SEARCH REPORT

International application No.

PCT/JP94/01916

## C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	Biochim. Biophys. Acta., Vol. 1089, 1991, Tamura, T. et al. "Molecular cloning and sequence analysis of cDNAs for five major subunits of human proteasomes (multicatalytic proteinase complexes)" p. 95-102	1-6 (775)
X	Mol. Cell. Biol., Vol. 3, 1983, Cowan, N. J. et al. "Expression of human alpha-tubulin genes: interspecies conservation of 3' untranslated regions" p. 1738-1745	1-6 (820)
X	Nucleic Acids Res., Vol. 17, 1989, Taaman, J. W. et al. "Nucleotide sequence of cDNA encoding subunit VIB of human cytochrome c oxidase" p. 1766-1766	1-6 (844)
X	Gene, Vol. 93, 1990 Taanman, J. W., Schrage, C., Ponne, N., Das, A., Bolhuis, P. A., de Vries, H. and Agsteribbe, E. Isolation of cDNAs encoding Subunit VIB of human cytochrome c oxidase and steady-state levels of coxVib mRNA in different tissues p. 285-291	1-6 (844)
X	J. Biol. Chem., Vol. 264, 1989, Gray, P. W. et al. "Cloning of the cDNA of a human neutrophil bactericidal protein: Structural and functional correlations" p. 9505-9509	1-6 (861)
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